

STIC Search Report Biotech-Chem Library

STIC Database Warking Number

TO: Nita M Minnifield

Art Unit: 1645

Location: rem/3C01/3C18 Serial Number: 09/970076

Friday, June 17, 2005

From: Beverly Shears

Location: Biotech-Chem Library

REM 1A54

Phone: 571-272-2528

beverly.shears@uspto.gov

Search Noises

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.



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ALIGNMENTS

Domain Domain Region Region Region Region Domain Protein Region 08-JAN-2003 ABP54903; Region Domain Peptide Homo sapiens Anthrax; toxin; Human anthrax toxin receptor. ABP54903 standard; protein; (first entry) receptor; human; antibacterial. /note= "forms metal ion-dependent amotif with amino acid residues 50, /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 50, 52, 54 and 150" /note= "forms metal ion-dependent amount with amino acid residues 50, /note= "forms metal ion-dependent adhesion motif with amino acid residues 50, 54, 118 /note= "forms metal ion-dependent adhesion motif with amino acid residues 52, 54, 118 /note= "PA-binding fragment, begins at any amino acid the range 27-43 and ends at any amino acid in the rang 221-321, region specifically described in Claim 3" /label= Signal_peptide 27. .321 /note= "putative transmembrane 28. .368 Location/Qualifiers note= "extracellular domain" note= "von Willebrand factor A domain" label= Mature_protein "cytoplasmic domain" 368 B domain" adhesion), 52, 118 adhesion site (MIDAS), 52, 54 and 118" site (MIDAS) and 150" site (MIDAS) and 150" site (MIDAS) and 150"

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tive 0; Mismatches
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A AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted compretent genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating cor ameliorating medical conditions, e.g., by protein or gene therapy. The protein in a sample or by determining the amount of the new genes. Specific uses are described for each of the 28 genes. The tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, autoimmune disorders, cancer, tumours, foetal and developmental abnormalities, autoimmune disorders, cancers, timestoja, inflammation, allergies, autoimmune cognitive disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., regnancy-related disorders, gastrointestinal disorders, gregnancy-related disorders, endocrine disorders, and infections. The proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a correct commonseasy or enzyme linked immunosorbent assay (ELISA). The invention can be used in alleviating of the invention in the invention of the invention of the invention of the invention of the invention.
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present sequence
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The present invention relates to albumin fusion proteins comprising a therappeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders
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25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
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albumin fusion proteins,

useful for diagnosing, treating,

preventing

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activities: Cytostatic, antianaemic, antiarthritic, antiasthmatic, anti-
CC HIV, immunosuppressive, antianaemic, antiavernic, antiasthmatic, antiacterial,
CC osteopathic, dermatological, antigut, immunomodulator, antiarrhythmic,
CC cardiant, nootropic, antilipaemic, nephrotropic, uropathic,
CC neuroprotective, antiparkinsonian, tranquilizer, antidiabetic, anabolic,
CC hypertensive, and vulnerary. The albumin fusion protein nucleic acid may
CC be used in gene therapy to treat disorders. The albumin fusion protein is
CC useful for diagnosing, treating, preventing or ameliorating diseases or
CC disorders comprising indication: V. The diseases or disorders include:
CC cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer),
CC immune or haematopoletic diseases (e.g. anaemia, Hodgkin's disease, acute
CC lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS,
CC autolmmune disease, inflammatory bowel disease, prostatitis, inguinal
CC disease), reproductive system disorders (e.g. prostatitis, inguinal
CC hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertoli-
CC leydig tumours), musculoskeletaci diseases (e.g. giant cell tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment or variant, a nucleic acid molecule comprising a polynucleotide sequence encoding the albumin fusion protein; a vector comprising the nucleic acid molecule of the albumin fusion protein; and a host cell comprising the nucleic acid molecule of the albumin fusion protein. The albumin fusion protein and its compositions have the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     albumin fusion protein formula; a method of treating a disease or disorder in a patient comprising the step of administering the albumin fusion protein; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; a method of extending the shelf life of Therapeutic protein: X, or its a method of extending the shelf life of Therapeutic protein: X, or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scleroderma, wound healing or epidermolysis bullosa). This sequence represents a therapeutic protein X relating to the albumin fusion prof the invention. The sequence listing data for this specification of the invention the USPTO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     further relates to: a composition comprising the albumin fusion protein and a pharmaceutical carrier; a kit comprising the composition of the
                                                  181
                                                                                                                                         147
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ALQGIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                               ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
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                                                                                                                                    ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
                                                                                                                                                                                                                                                                                                                  TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII
                                                                                                                                                                                                                                                                                                                                                                             TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1536; DB 8;
Pred. No. 1.8e-156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120

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RESULT 5
ABB90721
ABB9072
AX ABB9
AX Homo
AX ABB9
AX A
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Matches 295;
                            Query Match
Best Local :
                                                                                                                                                                                                                                     The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour provent, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriassis. Human, mouse and rat TEM genes and the encoded proteins (ABB9075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL9296-ABL92041 and ABL92143-ABL92191; normal
                                                                                                                                                                                                        endothelial markers (TEM) endothelial markers (NEM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-2000; 2000US-0222599P
11-AUG-2000; 2000US-0224360P
11-APR-2001; 2001US-0282850P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; necanglogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2002
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                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 209-210; 331pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200210217-A2
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                                                                                                                                                                                     ABL91903-ABL91995
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                            Similarity
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                                                                                                                     564 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinzler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endothelial
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               100.0%;
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(Σ,
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                                                                                                                                                                                                              ABL92042-ABL92074;
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0
                         Score 1536; DB 5
Pred. No. 3e-156;
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                                                                                                                                                                                                              pan-endothelial markers
                                                      Length
Indels
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Gaps
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RESULT 6
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11-AUG-2000;
11-APR-2001;
                                        The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90759 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL92042-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
                                                                                                                                                                                                                                                                                   An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                                                                                                                                                                                                                                                                                                                                                      St Croix B,
                                                                                                                                                                                                                                                     Disclosure; Page 136-137; 331pp; English
                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-291856/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antianglogenic; tumour; neoanglogenesis; vascularised tumour;
polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; mouse; rat; TEM; tumour endothelial marker; normal endothelial marker; pan-endothelial marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
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2000US-0224360P.
2001US-0282850P.
                                                                                                                                                                                                                                                                                                                                                                                      Kinzler KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endothelial Marker polypeptide SEQ ID NO 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
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                                                                                                                                                                                                                                                                                                                                                                                    Vogelstein
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immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic;
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Query

100.0%;

Score 1536;

DB 5

Length

Claim 1; Page 37-39; 45pp; English

human

animal suffering

Novel isolated polypeptide useful for identifying reduces effect of anthrax toxin on host cell, for

agent that prevents or treating human or non-

Sequence

564

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ABL91903-ABL91995

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RESULT 7
ABP54904
ID ABP5
XX ABP5
Y PT Poma
FT Prot
FT Poma
FT Doma
FT
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                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2001; 2001WO-US030941
                                                                                                                                                                                                                                         Young JAT,
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  11-APR-2001;
06-FEB-2002;
                                                                                    10-APR-2002;
                                                                                                                                            24-OCT-2002
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Pred. No. 3e-
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                                                            Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; neoangiogenesis; immune response; cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
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Pred. No. 3e-156;
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               Human heat mitochondrial protein as
                                              06-MAY-2004
                                                                                                       ADJ70017 standard; protein; 564
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Pred. No. 3e-156;
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17-JUN-2002;
20-SEP-2002;
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                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                mitochondrial protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function,
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                                                                                                                              TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
ALQGIIHSILKKSCIBILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                                                                                                                    564 AA;
                                                                                                   TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII
                                                                                                                                                               GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
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2002US-0389987P.
2002US-0412418P.
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                                                                                                                                                                                                                                                                                          The present invention describes a method for detecting a pancreatic CC cancer-associated transcript in a biological sample. The method comprises CC contacting the biological sample with a polynucleotide that selectively hybridises to a sequence at least 80% identical to a sequence as shown in CC any one of Tables 3 to 25 in the specification or having the GenBank Accession Number AF279145. Also described: (1) diagnosing pancreatic CC cancer in a human or animal subject being tested, determining the CC likelihood that a subject having a pancreatic cancer for CC surgical resection therapy; (2) detecting a pancreatic cancer associated polypeptide in a biological sample; (3) determining the likelihood that a subject having a pancreatic cancer. A pancreatic cancer associated colypeptide in a biological sample; (3) determining the likelihood that a colypeptide in a biological sample; (3) determining the likelihood that a subject having a pancreatic cancer. A pancreatic cancer and (4) monitoring the colypeptide or a therapeutic treatment of pancreatic cancer. A pancreatic cancer associated in CC gene and protein therapy. A pancreatic cancer associated transcript CC cancer associated transcript has cytostatic cancer associated transcript CC used for diagnosing or prognosing the polymucleotide, an isolated colypeptide or an antibody that binds to the isolated polypeptide can be used for diagnosing or prognosing pancreatic cancer or for preparing a colypeptide can be used for diagnosing or prognosing pancreatic cancer or for preparing a colypeptide cancer and for the early detection of pancreatic cancer or for preparing a colypeptide cancer for following the polymosic or the prognosic or the prognosic or the prognosic or concernation or following the polymosic or the prognosic or concernation or following the polymosic or the prognosic o
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                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
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                                                                                                                                                                                                   during remission or following surgery or chemotherapy. The present quence represents human tumour endothelial marker 8 precursor (TEM8 ich is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2004-635591/61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer-associated transcript; pancreatic cancer;
   100.0%;
llarity 100.0%;
Conservative 0
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   Score 1536; DB 8
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Indels

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Gaps

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551

The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 Ig mutated fusion protein of the invention.

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ARESULT 12
AD100550
ID AD100550
AC AD100
AC AD10
                                                                                                                                                                                                                                                                                                                                             New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-lik domain (VWF) amino acid sequence and an amino acid sequence heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cutaneous; inhalation anthrax; human; plasmid p0610; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion; von Willebrand factor A-like domain; vWF; cutaneous; inhalation anthrax; human; TANGO 197 Iq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rottman JB,
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                                                                                                                                                                                                                                                                      Claim 45; SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OZKA/)
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HEALEY J J.
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O'KEEFE T L.
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Best Local
                                                                                                                                                         domain (vWF) to the vWF.
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                                                                                                                                                                              New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing smellorating symptoms of anthrax comprises a von Willebrand factor domain (vWF) amino acid sequence and an amino acid sequence hetero
                                                                                                                                                                                                                                                                                  WPI; 2003-829643/77.
N-PSDB; ADM64575.
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The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ROTT/)
                                                                                                 Claim 44; SEQ ID NO 18; 64pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; cell culture; endocrine disorder; infection; wound healing; vulnerary; cell culture;
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                             Misc-difference
                                                                                                                                                                                                  Misc-difference
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320
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'note= "Encoded
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CC The genes and their secreted proteins are useful for preventing, treating CC or ameliorating medical conditions, e.g., by protein or gene therapy.

CC Pathological conditions can be diagnosed by determining the amount of the conditions can be diagnosed by determining the amount of the conditions can be diagnosed by determining the amount of the conditions in the trisques in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative conditions in the diagnosis or treatment of proliferative conditions in the diagnosis or treatment of proliferative conditions in the diagnosis or treatment of proliferative conditions are discorders, diseases of the immune system, AIDS, autoimmune conditions are conditive discorders, diseases of the immune system, AIDS, autoimmune conditions and discorders, schizophrenia, asthma, skin discorders (e.g., conditive discorders, schizophrenia, asthma, skin discorders (e.g., conditive discorders, kidney discorders, gastrointestinal discorders, conditions also be used to aid wound healing and epithelial cell conditions. The conditions of prevent skin aging due to sunburn, to maintain organs to regenerate tissues, to identify their cognate ligands or binding conditions or supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or conditions mentioned above, and in diagnostic immunoassays e.g., radioinmunoassays or enzyme linked immunoasrbent assay (BIISA). The invention can a human secreted protein of the invention can be used in alleviating the invention of the invention can be used in alleviating the invention of the invention can be used an archerian of the invention can be used in alleviating the invention of the invention can be used in alleviating the invention of the invention can be used in alleviating the invention can be used to a condition of the invention can be used to a condition of the invention c
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Best Local :
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30-JUN-2000; 2000US-0215133P.
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Query Match Best Local Similarity

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                                                         The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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osteopathic; antiarthritic.
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6 homo sapien
7 rattus norv
9 homo sapien
8 halocynthia
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mytilus edu
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Q9p218	Q8ivx1 Q6pi59	091145	Q951i2	Q9e877	Q75r52	Q8c720	Q8cbt2	Q6dcq6	Q7rf52	œ	Q6mg73	Q9ji30
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ALIGNMENTS

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heleh F.,
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RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Brownstein M.J., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Tock. Natl. Acad. Sci. U.S.A Common Co
     Hillman R.T., Green R.E., Brenner S.E.;

"An unappreciated role for RNA surveillance,";

Genome Biol. 5:RESEARCH008.1-RESEARCH008.16 (2004).

Genome Biol. 5:RESEARCH008.1-RESEARCH008.16 (2004).

-i-FUNCTION: Cellular role is not yet known.

-i- SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis. Binding does not occur in the presence of calci-
-i-SUBCELLULAR LOCATION: Type I membrane protein (Probable).

-i- ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms-4;
Comment-Experimental confirmation may be lacking for son
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okumura K., Naq
Nakai K., Yada
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Togashi T., Oyama M., Hata
Mizushima-Sugano J., Satoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPLICE ISOFORM(S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100; Scobie H.M., Rainey G.J.A., Bradley K.A., Young J.A.T.; "Human capillary morphogenesis protein 2 functions as an anthra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH ANTHRAX
                                                                                                   TISSUE SPECIFICITY: Highly expressed in tundut not in normal endothelial cells.
DOMAIN: Binding to PA seems to be effected SIMILARITY: Belongs to the ATR family.
SIMILARITY: Contains 1 VMFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=1;
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                                                                                                                                                                                                                                        IsoId=Q9H6X2-4;
                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9H6X2-1; Sequence=Displayed;
Note=May be produced at very low levels due to
codon in the mRNA, leading to nonsense-mediated
                                                                                                                                                                                                                                                                                         IsoId=Q9H6X2-3;
                                                                                                                                                                                                                                                                                                                                         IsoId=Q9H6X2-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180forms;
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Oyama M., Hata H., Watanabe M., Komatsu T.,
ugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
Nakamura Y., Ohara O., Isogai T., Sugano S.;
ada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36:40-45 (2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                 Sequence=VSP_000444,
                                                                                                                                                                                                                                      Sequence=VSP_000448,
                                                                                                                                                                                                                                                                                   Sequence=VSP_000446,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOXIN.
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                                                                                                                                                                                                                                                                                                                                                                                         ry low levels due to a premature stop to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                   VSP_000445;
                                                                                                                                                                                                                                                                              VSP_000447;
                                                                                                                                                                                                                                      VSP_000449;
                                                                                                                                                                                                              tumor
                                                                                                                                                           through
                                                                                                                                                                                                           endothelial
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InterPro; IPRO0839; Anth C.
InterPro; IPRO08395; VWF A.
Pfam; PF05587; Anth Ig; T.
Pfam; PF05586; Anth C; 1.
Pfam; PF00592; VWA; 1.
SMART; SM00327; VWA; 1.
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CARBOHYD
CARBOHYD
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DOMAIN
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50234; VWFA; 1
                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK001463;
BC012074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF279145;
AF421380;
AK025429;
                                                     181
                                                                        147
                                                                                            121
                                  207
                                                                                                                                                                                        295;
                                                                                                              87
                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                   Similarity
                                                                                                                                                               GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRWSFIVFS
        LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDGS
                                             ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                   ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
                                                                                                                       TRGTTLMKLTEDREQIRQGLEELQKVLFGGDTYMHEGFERASEQIYYENRQGYRTASVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIX0002125; -.
                                                                         ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
                                                                                                              TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII
                                                                                                                                                    GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
                                                                                                                                                                                      100.0%;
nilarity 100.0%;
Conservative 0
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AAH12074.1;
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BAB15128.1;
                                   ILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
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1664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nt is not removed. Use e agreement (See '3@isb-e''
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ALT_FRAME.
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Cytoplasmic
VWFA.
                                                                                                                                                                                                                                                                                    Missing (1)
/FTId=VSP_
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/FTId=VSP_000445.
NEKPFSVEDTYLLCPAPILKEVGMKAALQV
                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                               Missing
                                                                                                                                                                                                                                                                            DGSILAIALLILFLL -> LHKIASGPTTAACME
                                                                                                                                                                                                                                                                                                                 WVSSTSGFKEGNSHPCLPARPHT
                                                                                                                                                                                                                                                                                                                                           /FTId=VSP_000444.
Missing (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                               EDDD -> NKIK (in isoform
                                                                                                                                                                                                                                                                                                                                                                        N-linked
                                                                                                                                                                                                                                                                                                                                                                                             N-linked
                                                                                                                                                                                                                                                                                                                                                                                                     Pro-rich.
                                                                                                                                                                                                                                                                                                                                                                                                              Asp/Glu-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anthrax toxin receptor 1. 
Extracellular (Potential).
                                                                                                                                                                                                                              /FTId=VSP_000449.
B118A00AD5DF2233
                                                                                                                                                                                                                                               /FTId=VSP 000448.
Missing (In isoform 4).
                                                                                                                                                                                                                                                                                                         /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
                                                                                                                                                                                                                                                                   isoform 4).
                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                1536; DB 1;
No. 2.4e-114;
                                                                                                                                                                                                                                                                                               (in isoform 3).
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(GlcNAc...) (Potential).
(GlcNAc...) (Potential).
(KIK (in isoform 2).
                                                                                                                                                                                                                                                                                      000447.
                                                                                                                                                                                                                                                                                                        000446
                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential)
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                                                                                                                                                                                                                              CRC64;
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RESULT 28
ATRI MOUS
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AC 09023
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AC 0003
AC 0
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RA Alkaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Betsel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Scherland T., Gariboldi M., Gissi C., Godzik A., Frazer K.S.,
RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pilai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sultena R., Takenaka Y., Taylor M.S., Tasadale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Satoo K.,
RA Miyazaki A., Sakai K., Sasaki D., Shimada K., Shimada S.,
RA Miyazaki A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Miyazaki A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Miyazaki A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Miyashizaki Y.,
Ra Miyas
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Q9CZ52;
28-FEB-2003
28-FEB-2003
05-JUL-2004
                                  This
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MEDLINE=21443260; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., 1
Kinzler K.W., St Croix B.;
"Call sures."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 88-562 FROM N.A. (ISOFORM STRAIN=C57BL/6J; TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cancer Res. 61:6649-6655(2001).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Antxr1; Synonyms=Atr,
Mus musculus (Mouse).
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28-FEB-2003 (Rel. 41, L
05-JUL-2004 (Rel. 44, L
Anthrax toxin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Binds to the protective antigen anthracis (By similarity).
                                                                                        SIMILARITY: Belongs to the ATR family. SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type I membrane ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                   Event-Alternative splicing; Named
                                  SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                             IsoId=Q9CZ52-1;
                                                                                                                                                        (BOId=Q9CZ52-2; Sequence=VSP_000450;
dote=No experimental confirmation available;
WAIN: Binding to PA seems to be effected through the VWA
r similarity).
         the
         Swige
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         Institute
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ght. It is produced through Bioinformatics and the EN
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         a collaboration -
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      outstation
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RESULT 3
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Best Local S
Matches 291
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InterPro; IPR008400; Anth Ig.
InterPro; IPR008390; Ant C.
InterPro; IPR002035; VWF_A.
Pfam; PF05586; Anth Ig; I.
Pfam; PF05586; Anth C.
Pfam; PF00598; VWA; 1.
                                                       ATRZ_HUMAN STANDARD; PRT; 489 AA. P58335, Q86UI1; Q8NB13; Q96NC7; 28-FEB-2003 (Rel. 41, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Anthrax toxin receptor 2 precursor (Capillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
Name=ANTXR2; Synonyms=CMG2;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF378762; AAL11999.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                  (CMG-2).
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by non-profit institutions as l
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                                                                                                                                                                                                                                                                                                                                                                                                                                          291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50234; VWFA; 1. ive splicing; Glycoprotein; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                      GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
                                                                                                                                                                                      LNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDGS
                                                                                                                                                                                                                                       ALQGIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                                                                                     ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
                                                                                                                                                                                                                                                                                                              ALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQ
                                                                                                                                                                                                                                                                                                                                        TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENSQGYRTASVII
                                                                                                                                                                                                                                                                                                                                                               TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII 120
                                                                                                                                                                                                                                                                                                                                                                                        GHGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHRFISPQLRMSFIVFS
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GRCINFTRVKSQPAKYPLNNTYHPSSPPPAPIYTPPPAP
HCPPPAPSAPTPPISSPSTLPPPQAPPPNRAPPPSRPPP
RPSV -> RFRGWRLTICLGSKHVHPGPHPVCAPPAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VWFA.
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPSV -> RFRGWRLTICLGSKHVHPGRHDKGPETPLLKQAWMFSSFLERAFQ (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asp/Glu-rich
Pro-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential
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Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6AC92049B4BB4F7C CRC64;
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                                                              morphogenesis
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                                                              protein-2)
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Bell S.E., Mavila A., Salazar R., Bayless K.J., Kanagala S., Bayless S.A., Davis G.E.;
"Differential gene expression during capillary morphogenesis collagen matrices: regulated expression of genes involved in membrane matrix assembly, cell cycle progression, cellular differentiation and G-protein signaling.";
J. Cell Sci. 114:2755-2773(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=14702039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Synovial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 78-489 FROM N.A. (ISOFORM 3), (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scobie H.M., Rain
"Human capillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=21539596; PubMed=11683410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
[1]
                                                                                                                       FUNCTION: Cellular role is not yet known.
SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis in a divalent cation-dependent manner, with the following preference: calcium > manganese > magnesium > z.
Seems to bind to collagen type IV and laminin.
                                                                                           SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2) Secreted (isoform 3). Isoform 1 is expressed at the cell surface while isoform 2 is predominantly expressed within the endoplasmin
                                                                         reticulum and not at the plasma membrane.
ALTERNATIVE PRODUCTS:
                                                                 Event-Alternative
                            IsoId=P58335-2;
                                              IsoId=P58335-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acad. Sci. U.S.A. 100:5170-5174(2003).
                                                                                                                                                                          36:40-45(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rainey G.J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                morphogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOI=10.1038/ng1285;
Sequence=VSP_008344, ental confirmation ava
                          Sequence=VSP_008343;
                                              Sequence=Displayed;
                                                                splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bradley K.A., Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND INTERACTION WITH
                                                                 Named isoforms=4;
 44, VSP 008345;
available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.A.T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew;
                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50234; VWFA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008399; InterPro; IPR002035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P58335-4; Sequence=VSP_008346;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed in colon, heart,
liver, peripheral blood leukocytes, placenta, &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the ATR fami
SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liver, peripheral blood leukocytes, placenta, skeletal muscle, small intestine and spleen.

DOMAIN: Binding to PA seems to be effected through the VWA domain.

SIMILARITY: Belongs to the ATR family.
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AK091721;
                                              180
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157; Conserv
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PF00092; VWA; 1
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                                                                                                                             STRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVI
                                                                                                                                                                        GQGG-RREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVF
  TLNEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
                                     QALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSV
                                                                    IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGF
                                                                                                                 SSQATIILPLTGDRGKISKGLEDLKRVSPVGETYIHEGLKLANEQI--QKAGGLKTSSII
                                                                                                                                                             GPGGLLRAQEQPSCRRAFDLYFVLDKSGSVANNWIEIYNFVQQLAERFVSPEMRLSFIVF
                       QALKGI INSTLAQSCTETLELQPSSVCVGEEFQIVLSGRGFMLGSRNGSVLCTYTVNETY
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AAP04016.1;
BAB70976.1;
BAC03731.1;
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                                                                                                                                                                                                          Score 790.5; DB 1
Pred. No. 8.9e-55;
4; Mismatches 81
                                                                                                                                                                                                                                                                                                               Missing (In isofo /FTId=VSP_008345.
                                                                                                                                                                                                                                                                                                                                                                       /FTId=VSP_008343.
TLDVSVSFNGGKSVISGSLIVTATECSNGIAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
Anthrax toxin receptor
Extracellular (Potentia
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                                                                                                                                                                                                                                                      /FTId=VSP_008346.
P -> A (in Ref. 3;
B9F679DB75B6E2B7
                                                                                                                                                                                                                                                                                                                                                            VTQAGVKWHDLTHCTFGLSGSGDPPTSAS
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ed (GlcNAc...) (
g (in isoform 2).
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechal S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

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Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gun
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Best Local &
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR008400; Anth Ig.
InterPro; IPR008399; Ant C.
InterPro; IPR008399; Ant C.
Pfam; PF05580; Anth Ig.
Pfam; PF05580; Anth Ig.
Pfam; PF05580; Anth Ig.
InterPro; IRVAN; 1.
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25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor.
SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6; TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6, TISSUE=Eye;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anthrax toxin receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00327; VWA;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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LFFYSBREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
                                                                   GDRYKIGKGLEDLKAVKPVGETYIHEGLKLANEQI--QNAGGLKASSIIIALTDGKLDGL
                                                                                                              EDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHED
                                                                                                                                                                                                       PSCKKAPDLYPVLDKSGSVANNWIBIYNFVHQLTERFVSPEWRLSFIVFSSQATIILPLT
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                                                                                                                                                                                                                                                                                                                                                                               Score 770; DB 2;
Pred. No. 3.9e-53;
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RESULT REPORT OF THE PROPERTY 
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                      REPUINE-20530913; PubMed=1076801; DOI=10.1101/gr.152600; WEDLINE-20530913; PubMed=11076801; DOI=10.1101/gr.152600; WEDLINE-20530913; PubMed=1107691; Nasahir T., Wasahir T., Harada A., A Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Washiwagi K., A Yamamoto R., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., A Pujiwake S., Inoue K., Togawa Y., Izawa M
   sequencing property sequencing property [6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUB=Testis; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDiprepare full-length cDNA libraries for rapid discovery of Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6J; TISSUE-Testis;
The PANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome b
60,770 full-length cDNAs,";
Nature 420:563-573(2002).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933430J11 product:hypothetical proline-rich regi
Willebrand factor type A domain containing protein, full insert
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STRAIN=C57BL/GJ; FISSUE=Testis;
STRAIN=C57BL/G5; FISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
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Mammalia; Eutheria;
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Rodentia;
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Sciurognathi; Muridae;
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based on functional
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; Murinae; Mus
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annotation
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RESULT
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RC STRAIN=C57BL/6J; TISSUE=Testis;

RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

RA Adachi J., Aizawa K., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Horif F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Horif F., Imotani K., Ishii Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurbh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohasto N., Okazaki Y.,

RA Nishi K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Saito R., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahashi F., Takaki-Akahira S., Takeda Y., Tanaka T.,

RA Tagawa A., Taya T., Yasunishi A., Muramateu M., Hayyashizaki Y.;

RI Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

DR GO; GO:0016021; C:Integral to membrane; IEA.

DR GO; GO:004872; F:receptor activity; IEA.

DR Ffam; PF05587; Anth Ig; I.

DR Pfam; PF05587; Anth Ig; I.

DR Pfam; PF05092; VWA; I.

DR Pfam; PF05092; VWA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                       Q96EC6; PRELIMINARY;
Q96EC6;
01-DEC-2001 (TrEMBLrel. 1:
01-DEC-2001 (TrEMBLrel. 1:
01-OCT-2003 (TrEMBLrel. 2:
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
                                                                                                                                                                                                                                                                                                                                                                     ANTXR1 protein (Fragment).
Name=ANTXR1;
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50234; VWF
Hypothetical protein.
SEQUENCE 641 AA; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00453; VWFADOMAIN.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                      TISSUE=Breast;
                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLFFYSERBANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPYLDTMEEAKKARRMGAIVYTVGVFMYSKQQLVNIAGDPDRCFGVDEGFSALEGVVDPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDDCQGIFDLYLVLDKSGSVADNWIHIYSFAEGLVKKFTNPNLRISIITYSTEAEVILPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSKSCTEILSVQPTYVCAKDFYQVNISGHGLNNTSNMKQVICRFKFSDSKVVDESPSDMN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSDSKEINKSLLVLKSIVPQGLTHMQKGLRKANEQIRKSTLGGRIVNSVIIALTDGLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHSITCPGPKIKHTGEDVSLQVSLNNGISFIGNKLIITSTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHE
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                                                                                                                                                                                                                                                                                                                                                                                                                          19,
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                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                             Craniata; Vertebrata; E
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                   Homo
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2001) to the EMBL/GenB Submitted (AUG-2001) to the EMBL/GenB EMBL; BC012475; AAH12475.1; -. GO; GO:0016021; C:integral to membran GO; GO:0004872; F:receptor activity; InterPro; IPR008400; Anth_Ig.
Pfam; PF05587; Anth_Ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diatchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G., Bhakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.T., Marra M.A., Shailus D.E., Schnerch A., Schein J.E., Jones S.T., Marra M.A.
                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PI
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                      "Cloning of rat alpha D, a novel beta 2 integrin."; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                              O'Brien M.M.,
                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9QYE7;
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                                                                                                                                                                                                                            Gallatin W.M.
                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                          Integrin alpha-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IISSUE=Breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAD RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of bloodborne pathogens, particulate matter, and senescent erythrocytes from the blood (By similarity).

SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).

SUBCELIULAR LOCATION: Type I membrane protein (By similarity).

DOMAIN: The integrin I-domain dinsert) is a VWFA domain. Integrin with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                            VanderVieren M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA; 10453 MW;
                                                                                                                                                                                                                                                                                                                                                                                             precursor.
                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.3%;
95.1%;
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Pred.
                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                          Kilgannon P.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388; DB 2;
No. 1.9e-23;
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                                        Integrins
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SIMILARITY: Contains 7 FG-GAP repeats. SIMILARITY: Contains 1 VWFA domain.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Signal;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calcium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00242; INTEGRIN ALPHA; PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; BM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF A.
Pfam; PF01839; PG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF021334; AAF21241.1; -. HSSP; P11215; 1BHQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
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                                                                                                     Match
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  212
                                                            18
                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Swiss Institute of Bioinforma
ean Bioinformatics Institute. Th
non-profit institutions as long
 DPOSLVDPIVQLO
                  DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED
                                       DIAFLIDGSGSINGRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL
                                                           DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adhesion; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane
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1045
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402
454
577
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775
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1017
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89
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1100
1121
1161
87
                                                                                        10.4%;
GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
                                                                                41;
                                                                                                                               GFFKR motif.
By similarity.
N-linked (GlcNAC.
                                                                                                                                                                                                                                                                                                                                          Potential.

Cytoplasmic (Potential).
FG-GAP 1.
FG-GAP 2.
VWFA.
FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 6.
FG-GAP 6.
FG-GAP 7.
Potential.
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:
                                                                               Score 159.5;
Pred. No. 0.00
11; Mismatches
                                                                                                                                                                                                                                                                                                                        Potential.
Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Integrin; Magnesium; Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There
                                                                                          ; DB 1;
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                                                                                                  Length
                                                                                                                        CRC64;
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RESULT
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Q13349; Q15575; Q15576;
16-OCT-2001 (Rel. 40, Create
16-OCT-2001 (Rel. 40, Last s
05-JUL-2004 (Rel. 44, Last a
Integrin alpha-D precursor (
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HUMAN
                                                                                                                                                                       binding interface between I domain and VCAM-1.";

7. Immunol. 163:1984-1990(1999).

-i- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and

VCAM1. May play a role in the atherosclerotic process such as

clearing lipoproteins from plaques and in phagocytosis of blood-
borne pathogens, particulate matter, and senescent erythrocytes
                                                                                                                                                                                                                                                                                                                                MEDLINE=99370002; PubMed=10438935;
Van der Vieren M., Crowe D.T., Hoekstra D.,
Grayson M.H., Bochner B.S., Gallatin W.M., S
"The leukocyte integrin alpha D beta 2 bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99059842; PubMed=9841932;
Grayson M.H., Van der Vleren M., Sterbinsk
Hoffman P.A., Staunton D.B., Bochmer B.S.;
"alphadbeta2 integrin is expressed on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20187620; PubMed=10722744; DOI=10.1074/jbc. Noti J.D., Johnson A.K., Dillon J.D.; "Structural and functional characterization of the gene CD11d. Essential role of Spl and Sp3."; J. Biol. Chem. 275:8959-8969(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96111956; PubMed-8777714; DOI-10.1016/1074-7613(95)90058-6; Van der Vieren k. Le Trong H., Wood C.L., Moore P.F., St John T., Staunton D.E., Gallatin W.M.; Staunton D.E., Gallatin W.M.; Ta_novel leukointegrin, alpha d beta 2, binds preferentially to ICAL, "A_novel leukointegrin, alpha d beta 2, binds preferentially to ICAL."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96257236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=ITGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERACTION WITH VCAM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTION WITH VCAM1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF
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from the blood.
SUBUNIT: Heterodimer of an alpha and associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane TISSUE SPECIFICITY: Expressed moderat lines and subsets of peripheral blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an alternative
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171:291-294(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Med. 188:2187-2191(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F 467-537; 571-602; 633-666; 788-834 AND 910-1125 FROM N.; 257236; PubMed-8666289; DOI=10.1016/0378-1119(95)00869-1; Davis E.M., LeBeau M., Springer T.A.; nd chromosomal localization of a novel gene-encoding a human company of the company of the control of the 
                     AR LOCATION: Type I membrane protein.
ECIFICITY: Expressed moderately on myelomonocytic cell
subsets of peripheral blood leukocytes and strongly o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ligand
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed on human eosinophils and for vascular cell adhesion molecule
                                                                                                                                                                                                                                                                                                        lpha D beta 2 binds VCAM-1:
I domain and VCAM-1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    annotation update)
(Leukointegrin alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sterbinsky
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                                                                                                                                 beta subunit.
                                                                                                                                                                                                                                                                                                                                                           Vazeux R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukocyte integrin
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; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecule
                                                                                                                                                                                                                                                                                                                                      evidence
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                                                                                                                              Alpha-D
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and strongly on

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EMBL; U37028; AAB38547.1; -.
EMBL; U40274; AAB60634.1; -.
EMBL; U40275; AAB60635.1; -.
EMBL; U40276; AAB60637.1; -.
EMBL; U40277; AAB60637.1; -.
EMBL; U40279; AAB60638.1; -.
EMBL; U40279; AAB60638.1; JOIN
EMBL; D40278; AAB60638.1; JOIN
EMBL; AF187881; AAF62875.1; -.
HSSP; P11215; 1BHQ.
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PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int alpha; 15
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01839; FG-GAP; 3.
Pfam; PF000357; Integrin_alpha;
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0008305; C:integrin complex; TAS.
GO; GO:0016337; P:cell-cell adhesion; NAS.
GO; GO:0007160; P:cell-matrix adhesion; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF A.
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                                                                                                                                                                               REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue-specialized cells, including macrophages foam cells within atherosclerotic plaques, and on splenic red pulp macrophages. DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrine with I-domains do not undergo protease cleavage. SIMILARITY: Belongs to the integrin alpha chain family. SIMILARITY: Contains 7 G-GAP repeats. SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European
                                                                                                                                                                                                                                                                                                                              SM00191; Int_alpha; 5.
SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC: 6146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (See http://www.isb-sib.ch/announce, an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       Signal;
  ROT entry is copyright. It is produced through Swiss Institute of Bioinformatics and the EM Bioinformatics Institute. There are no restructed institutions as long as its content
                                                                                                                                                                                                                                                                                         Transmembrane
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                                                                                                                                               Potential.

Cytoplasmic (Potential).

FG-GAP 1.

FG-GAP 2.

VWFA.

FG-GAP 3.

FG-GAP 4.

FG-GAP 5.

FG-GAP 6.

FG-GAP 7.

FG-GAP 7.

FG-GAP 7.

FG-GAP 7.

FG-GAP 7.

FG-GAP 7.

FG-GAP 7.
Potential.
Potential.
GPFKR motif.
By similarity.
N-linked (GlcNAc.
N-linked (GlcNAc.
N-linked (GlcNAc.
N-linked (GlcNAc.
N-linked (GlcNAc.
                                                                                                                                                                                                                                                            Extracellular (Potential)
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                                                                                                                                                                                                                                                                      Integrin alpha-D.
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                                                                                       Q9BPQ8;
Q9BPQ8;
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01-JUN-2001 (TrEMBLrel. 17, I
01-JUN-2003 (TrEMBLrel. 24, I
Integration alpha Hrl precursor.
                                                                                    -|- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-|- SIMILARITY: Belongs to the integrin alpha chain family.
EMBL; AB048261; BAB21479.1; -.
HSSP; P11215; 18HQ.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0003105; C:integral to membrane; IEA.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0007120; P:cell-matrix adhesion; IEA.
GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
                                                                                                                                                                                           Miyazawa S., Azumi K., Nonaka M.; "Cloning and characterization of integrin alpha solitary asoldian, Halocynthia roretzi."; J. Immunol. 166:1710-1715(2001).
                                                                                                                                                                                                                                                                                                 Name=HrITGAl;
Halocynthia roretzi (Sea squirt).
Bukaryota, Metazoa, Chordata, Urochordata, Ascidiacea,
Stolidobranchia, Pyuridae, Halocynthia.
         PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOMAIN
SMART; SM00191; Int_alpha; SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                          TISSUE=Hemocyte;
MEDLINE=21103187; PubMed=11160215;
                                                                                                                                                                                                                                                                                   NCBI_TaxID=7729;
                                                        Pfam; PF00092; VWA;
                                                                 InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.
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N-linked (GlcNAc...)
N-linked (GlcNAc...)
N-linked (GlcNAc...)
N-linked (GlcNAc...)
N-linked (GlcNAc...)
L-v (in Ref. 2).
V-> A (in Ref. 2).
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                       sequence update) annotation updat
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) (Potential).
) (Potential).
) (Potential).
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ID QBNFW1
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ID QBNFW
AC QBNFW
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Query Match
Best Local Similarity
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Best Local
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InterPro; IPR008985; Cona like_]
InterPro; IPR003129; TSP_N.
InterPro; IPR003129; VWF_A.
Pfam; PF01391; Collagen; 16.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8NFW1;
Q8NFW1;
01-OCT-2002
01-OCT-2002
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P18614; 1MHP.
Genew; HGNC:22989; COL22A1.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005198; F:structural molecule activity;
GO; GO:0005198; P:cell adhesion; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
InterPro; IPRO08161; Cly_helix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1 type XXII collagen.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell adhesion; Integrin; Signal; Transmembrane.
SIGNAL 1 30 Potential.
CHAIN 31 1332 integrin alpha Hrl
                                                                                                                                                                                PRINTS; PRO0453; VWFADOMAIN.
ProDom; PD000007; Clg_helix;
SMART; SM00210; TSBN; 1.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koch M., Jin W., Ashworth T., Burgeson R.E.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
FMBT. 156-67994
                                                                                                                               PROSITE; PS50234; VWFA; 1. Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Cartilage;
Koch M., Jin W., Ashworth T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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1332 AA;
     Conservative
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                                                                                                      161115 MW;
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9.7%; Score 148.5; DB 25.4%; Pred. No. 0.0091; ive 45; Mismatches 10
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W; OD9108D2B05CFFAE
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  105;
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  Indels
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                                                   1626;
41;
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Gaps
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Best Local Similarity
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01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Proximal thread matrix protein 1 variant a.
Myrilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomory
Myrtloidea; Myrilidae; Myrtlius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomacromolecules 3:1240-1248(2002).
EMBL; AP414454; AAL63537.1; -.
GO; GO:0005198; F:structural molecul.
InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Collagen-binding matrix proteins byssal fibers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903; Sun C., Lucas J.M., Waite J.H.;
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TSSFNKLSKIMENVVKLACM
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                                                             NDGFQALQGIIHSILKKSCI
                                                                                                                       VILLTDGQNNGHKS----PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-T
                                                                                                                                                                                 IIALTDGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.6%; Score 148; DB 2; Length 441; ilarity 25.5%; Pred. No. 0.002; Conservative 46; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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RESULT Q8T5C3

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01-JUL-1989
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MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903;
Sun C., Lucas J.M., Waite J.H.;
                                              MEDIINE-8831503; PubMed=2457584; Corbi A.L., Kishimoto T.K., Miller L.J., Sp "The human leukocyte adhesion glycoprotein type 3, CD11b) alpha subunit. Cloning, prim to the integrins, von Willebrand factor and J. Biol. Chem. 263:12403-12411(1988).
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01-JUL-1996 (Rel. 34, Last sequence update)
01-OCT-2094 (Rel. 45, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein subunit) (Re.3 alpha chain) (CD11b) (Leukocyte adhesic
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SEQUENCE 444
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byssal fibers.";
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Mytiloidea; Mytilidae; Mytilus.
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01-JUN-2002
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GO; GO:005198; F:structural
InterPro; IPR002035; VWF_A.
Pfam; PF00092; VWA; 2.
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  SEQUENCE
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                               Name=ITGAM; Synonyms=CD11B,
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                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                           (Neutrophil adherence receptor)
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002 (TrEMBLrel. 21, Last s
003 (TrEMBLrel. 24, Last a
thread matrix protein 1b.
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  FROM N.A
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                                                                                                                                                                                                                                                                                                                          (Human)
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Pred. No. 0.002;
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                                                                                                                                                 Springer T.A.;
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X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.

MEDLINS=98362595; PubMed=9867375; DOI=10.1016/S0969-2126(98)00093-8; Baldwin E. T., Sarver R.W., Bryant G.L. Jr., Curry K.A., Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L., Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E., Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.; "Cation binding to the integrin CD11b I domain and activation model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87076671; PubMed=3539202; DOI=10.1016/0167-4838(86)90037-3; pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.; "N-terminal sequence of human leukocyte glycoprotein Mo1: conservat: across species and homology to platelet IIb/IIIa."; Biophys. Acta 874:368-371(1986).
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MEDLLINE=88257215; PubMed=2454931; DOI=10.1

Arnaout M.A., Gupta S.K., Pierce M.W., Ten

"Amino acid sequence of the alpha subunit

receptor Mo1 (complement receptor type 3).

J. Cell Biol. 106:2153-2158(1988).
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Arnaout M.A., Remold-0'Donnell E., Pierce M.W., I Arnaout M.A., Remold-0'Donnell E., Pierce M.W., I "Molecular cloning of the alpha subunit of human leukocyte adhesion glycoprotein Mo1: chromosomal homology to the alpha subunits of integrins.";
Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
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MEDLLNB=96363671; PubMed=8747460; DOI-10.1016/S0969-2126(01)00271-4;
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"Two conformations of the integrin A-domain (I-domain): a pathway fo:
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MEDLLNB=95171458; PubMed=7867070; DOI=10.1016/0092-8674(95)90517-0;

MEDLLNB=95171458; PubMed=7867070; DOI=10.1016/0092-8674(95)9051
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"The promoter of the CD11b gene directs
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Pierce M.W., Tenen D.G.;
ne alpha subunit of human leukocyte adhesion
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Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875 (1998).

-I- FUNCTION: Integrin alpha-M/beta-2 is implicated in various adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles. It is identical with CR3 receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for fibringen, factor X and ICAM1. It recognizes P1 and P2 peptides
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"Experimental support for a beta-propeller domain in integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxvig C.,
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Structure 6:923-935(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              granulocytes.

DOMALN: The integrin I-domain (insert) is a VWFA domain with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 7 FG-GAP repeats.

SIMILARITY: Contains 1 VWFA domain.

SIMILARITY: Contains 1 VWFA domain.

DATABASE: NAME-PROW; NOTE-CD guide CD11b entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd11b.htm".
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SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Predominantly expressed in monocytes and
                                                            J03925 AAA594911;
J04145 AAA59993.1;
J04145 AAA59993.1;
S52227 AAB24821.1;
S52153 AAB24821.1;
S52154 AAB22821.1;
S52155 AAB22821.1;
S52157 AAB24821.1;
S52159 AAB22821.1;
S52161 AAB22821.1;
S52167 AAB22821.1;
S52167 AAB22821.1;
S52169 AAB22821.1;
S52170 AAB22821.1;
S52170 AAB22821.1;
S52170 AAB22821.1;
S52171 AAB22821.1;
S52171 AAB22821.1;
S52171 AAB22821.1;
S52172 AAB22821.1;
S52173 AAB22821.1;
S52174 AAB22821.1;
S52175 AAB22821.1;
S52175 AAB22821.1;
S52176 AAB22821.1;
S52177 AAB22821.1;
S52177 AAB22821.1;
S52177 AAB22821.1;
S52217 AAB22821.1;
S52217 AAB22821.1;
S52217 AAB22821.1;
S52221 AAB22821.1;
S52222 AAB22821.1;
S52222 AAB22821.1;
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Best Local
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GO; GO:0007155; P:cell adhesion; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWP_A.
Pfam; PF01039; FG-GAP; 3.
Pfam; PF000357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                          Q8T5C2 PRELIMINARY; PRT; 453 AA.
Q8T5C2;
Q8T5C2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 24, Last annotation update)
Proximal thread matrix protein 1.
Mytilus galloprovincialis (Mediterranean mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphi
Mytiloidaa; Mytilidae; Mytilus.
                                      SEQUENCE FROM N.A.

MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903;
Sun C., Lucas J.M., Waite J.H.;

"Collagen-binding matrix proteins from elastomeric extraorganismic byssal fibers.";
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-structure; Calcium; Cell adhesion; Direct Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00242; INTEGRII PROSITE; PS50234; VWFA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                              NCBI_TaxID=29158;
lomacromolecules 3:1240-1248(2002)
MBL; AY053391; AAL17974.1; -.
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X-ray;
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@=143-334.
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Pred. No. 0.01;
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Repeat; Signal;
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RESULT 15
ITAX HUMAN
ID ITAX
AC P2070
AC P2070
DT 01-FF
DT 05-FF
RT 7-CDNJ
RA COZD-J
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Best Local 9
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausmer R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-8816645; PubMed-3327687;

CODIA A.L., Miller L.J., O'Connor K., Larson "CDNA cloning and complete primary structure leukocyte adhesion glycoprotein, p150,95.";

EMBO J. 6:4023-4028(1987).
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SMART; SM00327; VWA; 2.
PROSITE; PS50234; VWFA; 2.
                                                                                                                                                                                                                                                                                                    ERRATUM.
Corbi A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002035; Pfam; PF00092; VWA; 2
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Homo sapiens (Human)
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                                                                                                                                                                MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                              SEQUENCE FROM TISSUE-Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90153906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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L., Garcia-Aguilar J., Sp.
structure of an integrin
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                                                                                                                                                                                                                                                                                                                                                                                        Chem.
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                                                                                                                                                                                                                                                                             Garcia-Aguilar J., Springer T.A.;
sm. 265:12750-12751(1990).
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                                                                                                                                                                                                                        N.A.
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MIM; 151510; -. GO; GO:0008305; (GO:0004872; EGO; GO:0007155; EGO; GO:0009887; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF
                                                  PRINTS; PR01185; INTEGRINA. PRINTS; PR00453; VWFADOMAIN.
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InterPro; IPR002035; VWF_A.
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MEDLINE=87167596; PubMed=3549901;
                                                                                                                                                                                                                                                                      Genew;
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                                                                                                                                                                                                                                                                                                      PIR; A36584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Integrin alpha-X/beta-2 is a receptor for i recognizes the sequence G-P-R in fibrinogen. It media interaction during inflammatory responses. It is espe important in monocyte adhesion and chemotexis.

SUBUNIT: Heterodimer of an alpha and a beta subunit.
                                                                                                                                                                                                                                                                                                                                      L; M81695; AAA59180.1; —
L; M29165; -; NOT ANNOTATED CDS.
L; M29487; AAA51620.1; JOINED.
L; M29483; AAA51620.1; JOINED.
L; M29483; AAA51620.1; JOINED.
L; M29485; AAA51620.1; JOINED.
L; M29485; AAA51620.1; JOINED.
L; M29485; AAA51620.1; JOINED.
L; M29486; AAA51620.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain famil
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
DATABASE: NAME=PROW; NOTE=CD guide CD11c entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd11c.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        granulocytes.

DOMAIN: The integrin I-domain (insert) is a VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein TISSUE SPECIFICITY: Predominantly expressed
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[mmunol. 138:2381-2383(1987)
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                                                                                     PF01839; FG-GAP; 3.
PF00357; Integrin_alpha;
PF00092; VWA; 1.
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SM00327;
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HGNC:6152; ITGAX.
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an email to license@isb-sib.ch).
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                     GAGAGTGAGGAAAATAAAATAAAA
                                                                                              TGGTTCTGGCCCCCTCTGCACTGTGATTATCAAGGAGGTCCCTCCACCCCCCTGCCGAG
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2 (bases 1 to 1414)
Bradley,K.A., Mogridge,J.,
Direct Submission
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1 (bases 1 to 1414)

Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.

Identification of the cellular receptor for anthrax toxin

Nature 414 (6860), 225-229 (2001)
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TYLLCPAPILKEVGNKAALQYSMNDGLSFISSSVIITTTHCSDGSILAIALLILFLLL
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AX393246 LOCUS AX393246 AX393246 Sequence 176 from Patent WO0210217. ACCESSION AX393246 VERSION AX393246 VERSION AX393246.1 GI:19701296 KEYWORDS SOURCE ORGANISM Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; REFERENCE AUTHORS TITLE JOURNAL THE Endothelial cell expression patterns Patent: WO 0210217-A 176 07-FEB-2002; FEATURES Location/Qualifiers 5540 bp DNA linear PAT 23-MAR-2002 DATE 23-MAR-2002 FALTICE STORMAL The Johns Hopkins University (US) Location/Qualifiers	QY 1021 TGGTTCTGGCCCCTCTGCTGCACTGTGATTATCAAGGAGGTCCCTCCACCCCTGCCGAG 1	901 GATGGCCTCTTTTATCTCCAGTTCTGTCATCACCACCACCACACTGTTCTGACGGT	OY /21 GIGAGAGAAACGGCTTCCGACATGCCCCCAACGTGGACACGGGTCCTCTGCAGCTTCAAG	601 GTGAATGACGCCTTTCAGGCTCTGCAAGGCATCAACTCAATTTTGAAGAAGTCCTGC	Qy 421 ACAGCCAGCGTCATCATTGCTTTGACTGATGAGAACTCCATGAAAGATCTCCTTTTTCTAT 4	Db 404 CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG 4 Oy 361 CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAACAGACAAGGGTACAGG 4
Db 804 ATCGAAACTGCTGGCACATGCCACCACACGGGAGGTCCACCACGGTCAGCTTCAAG Qy 721 GTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAG B64 GTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAG Db 864 GTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAG Qy 781 ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGACACTTATTTACTG Db 924 ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGACACTTATTTACTG Qy 841 TGTCCAGCGCCTATCTTAAAAGAAGTTGGCATGAAAGCTGCACCACGGTCAGCATGAAC Qy 901 GATGGCCTCTCTTTAAAAGAAGTTGGCATGAAAGCTGCACCACCACGTCAGGACATGAAC Qy 901 GATGGCCTCTCTTTTATCTCCAGGTTCTGTCACCACCACCACACTCTTCTGAACGT Db 1044 GATGGCCTCTCTTTTATCTCCAGGTTCTGTCATCACCACCACACACTGTTCTGACCGT		Qy 421 Db 564 Qy 481 Op 624	384 301 444 361	Qy 121 GGCGGATTTGACCTGTACTTCATTTTGGACAATCAGGAAGTGTGCTGCACCACTGGAAT 180	Query Match Best Local Similarity 99.88; Pred. No. 0; Best Local Similarity 99.88; Pred. No. 0; Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0; 1 ATGGCCACGGCGAAGCCGAAGCCCTCGGCATCGGCTTCCAGTGGCTCTTTTGGCCACT 60	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

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AX393301.1 GI:19701322
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, I
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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                                                                ACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAACTCCATGAAGATCTCTTTTTCTAT
                                                                                                                                              CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAACAGACAAGGGTACAGG
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 5 from E
AX458370
AX458370.1 GI:21
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Receptor for b. Anthracis toxin
Patent: WO 0246228-A 5 13-JUN-2002;
WISCONSIN ALUMNI RESEARCH FOUNDATION
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Mammalia; |
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                                                                                                                                                                                                                                                                                                , Metazoa;
Eutheria;
/codon_start=1
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/db_xref="GI:21725041"
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/mol_type="unassigned DN/
/db_xref="taxon:9606"
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                                                                                                 note="unnamed protein product"
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Primates;
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RMEVRWGEKGSTEEGGAKLEKAKNARVKWPEQDSTEFPERNLNNMRRPSSPFRKKYSPJI
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            TGTCCAGCGCCTATCTTAAAAGAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC
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Submitted (16-JUN-2000) Johns Hopkins Oncology Center, Hopkins University, 1650 Orleans Street, Baltimore, MD (bases 1 to 5540)
St. Croix, B., Vogelstein, B. and Kinzler, K.W. Direct Submission
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Science 289 (5482), 1197-1202 (2000)
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St. Croix, B., Rago, C., Velculescu, V.,
Montgomery, E., Lal, A., Riggins, G.J., I
Kinzler, K.W.
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Mammalia; Eutheria; Primates;
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                                              /translation="MATAERRALGIGFOWLSLATIVLICAGQGGRREDGGPACYGGFD
LYFILDKSGSVLHHWMBIYYFVBQLAHKFISDREQI
RQGLEBLQKYLPGGDTYMHKGFERASEQIYEMERGYBTASVIIALTDGBELHBULFFY
SEREANRSRDIGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKK
SCIBILABLSTICAGSSFQVVVRGNGFRHAKNVDRVLCSFKLDSVTLNEKFPSVED
TYLLCPAFILKEVGNKALQVSKNDGLSFISSSVIITTHGSDGSILATILLILFLLL
ALALLWHFWPLCCTVIIKEVPPPPAEESEEEDDDGLFKKKWPTVDASYYGGRGVGGIK
RMEVRWGEKGSTEEGAKLEKAKNARVKMPEQEYEFPEPRNLINNNMRRPSSPRKWYSPI
KGKLDALWVLLRKGYDRVSVMRPQPGDTGRCINFTRVKNNQPAKYPLNNAYHTSSPPP
APIYTPPPPAPHCPPPPPSAPTPPIPSPPSTLPPPPQAPPPNRAPPPSRPPPRPSV"
                                                                                                                                                                   /gene="TEM8"
/codon_start=1
/product="tumor endothelial
/protein_id="AAK52094.1"
/db_xref="GI:14017381"
                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                               TCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTGTTTACTGTGTTGGTGTG
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/gene="TEM8"
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/product="tumor 6
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/gene="TEM8"
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TITLE
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Best Local Similarity 99.9
Matches 950; Conservative
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Receptor for b. Anthracis toxin
Patent: WO 024628-A 7 13-JUN-2002;
WISCONSIN ALUMNI RESEARCH FOUNDATION (U
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db_xref="taxon:9606"
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Magner, L., Shenmen, C.M., Schuler, G.D.,
Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Blatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
MCKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
                                                                                                                                                                                                                                                                                                                                                                         BC012074 2112 bp mRNA linear PRI 29-JUN-20 Homo sapiens anthrax toxin receptor 1, transcript variant 3, mRNA (CDNA Clone MGC:19967 IMAGE:4563020), complete cds.
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                       Homo sapiens
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cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLIL at: http://image.llnl.gov Series: IRAL Plate: 29 Row: g Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16933552.
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Submitted (02-AUG-2001) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Wadan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
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Contact: MGC help desk
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                                                                                                                                                                                                            /product="tumor endothelial m
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/clone lib="WIH MGC 14"
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Query Match Best Local Similarity

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Score 949.4; DB 9; Pred. No. 2.6e-272;

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St Croix, B., Kinzler, K.W. and Vogelst
Endothelial cell expression patterns
Patent: WO 0210217-A 186 07-FEB-2002;
The Johns Hopkins University (US)
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                    TGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAGATCAATGACTCGGTCACACTCAA
                                          ATCCACCATCTGCGCGGGAGAGTCCTTTCAAGTGGTCGTAAGAGGAAATGGCTTCCGACA
                                                      ATCCACCATATGTGCAGGAGAGTCATTTCAAGTTGTCGTGAGAGGAAACGGCTTCCGACA
                                                                                       GCAAGGCATCATCCACTCAATTTTGAAGAAGTCCTGCATCGAAATTCTAGCAGCTGAACC
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          TGCCCGCAATGTGGACAGGGTCCTCTGCAGCTTCAAAATCAATGACTCAGTCACGCTCAA
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/mol_type="unassigned DNI
/db_xref="taxon:1000"
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Pred. No. 1.8e-243;
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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2 (bases 1 to 5220)
Carson-Walter, E.B., Vogelstein, B., Ki
Direct Submission
Submitted (10-MAY-2001) Oncology, Jol
Orleans Street, Baltimore, MD 21231,
                                                                                                        Bukaryota; Metazoa; Chordata; Crar
Mammalia; Eutheria; Rodentia; Sciv
1 (bases 1 to 5220)
Carson-Walter, E.B., Watkins, D.N.,
Kinzler, K.W. and St Croix, B.
Cell surface tumor endothelial man
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21443268
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/prodoin_Btart=1
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/product="tumor |
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Tang, Y. T., Zhou, P. and Drmanac, R. T.
Nucleic acids and polypeptides
Patent: US 6569662-A 8 27-MAY-2003;
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Sequence 30:
CQ498433
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                                                                                                                                                                     Patent: WO 0160860-A 30300 23-AUG-2001, Millennium Predictive Medicine, Inc. (U Location/Qualifiers
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HELIX RESEARCH INSTITUTE
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PN JP 2002191363-A/11166
PD 09-JUL-2002
PF 28-JUL-2002
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Primer for synthesizing full-length cDNA and use thereof FH I
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG
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3 949	ATCAATGACTCGGTCACACTCAGTAAG	923	망
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GTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAG 922	GTGAGAGGNAACGGCTTCCGACATGCC	863	₽
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GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTTGAAGAAGTCCTGC 802	GTGAATGACGGCTTTCAGGCTCTGCAA	743	Db
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TCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTGTTTACTGTGTGTG	TCAGAGAGGGAGGCTAATAGGTCTCGA	481	ş
ACAGCTAGCGTCATCATTGCTTTGACTGATGGAGGACTCCATGAAGATCTCTTTTTCTAT 622	ACAGCTAGCGTCATCATTGCTTTGACT	563	В
ACAGCCAGCGTCATCATTGCTTTGACTGGAGAAGAACTCCCATGAAGATCTCTTTTTCTAT 480	ACAGCCAGCGTCATCATTGCTTTGACT	421	8
CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAAACAGACAAGGGTACAGG 562	CATGAAGGATTTGAAAGGGCCAGTGAG	503	Вb
CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATTATGAAAACAAGACAAGGGTACAGG 420	CATGAAGGATTTGAAAGGGCCAGTGAG	361	\$

Search completed: June 14, 2005, 15:32:17 Job time: 5150 secs



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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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949.4	949.4	949.4	950.8	950.8	952.4	952.4	952.4	952.4	960.8	960.8	1089.4	1090.6	1090.8	1090.8	1090.8	1090.8	1090.8	1090.8	1104	Score		
86.0	86.0	86.0	86.1	86.1	86.3	86.3	86.3	86.3	87.0	87.0	98.7	98.8	98.8	98.8	98.8	98.8	98.8	98.8	100.0	Match	*	•
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ADI00551	ADM64581	ADI00555	ADM64585	ADI00541	ADM64591	ADM64589	ADI00547	ADI00545	ADM64575	ADI00549	AAD05334	AAD05303	ADR48215	ABX72003	ABX72029	ABV73882	ABL92104	ABL92078	ABV73881	ID		SUMMARIES
Adi00551 Human TAN	Adm64581 Human TAN	Adi00555 Human TAN	Adm64585 TANGO197	Adi00541 Human TAN	Adm64591 TANGO197	Adm64589 TANGO197	Adi00547 Human TAN	Adi00545 Human TAN	Adm64575 Mouse TAN	Adi00549 Human TAN	Aad05334 Human sec	Aad05303 Human sec	Adr48215 Human tum	Abx72003 DNA encod	Abx72029 DNA encod	Abv73882 Human ant		Abl92078 Human Tum	3	Description		

Novel isolated polypeptide useful for identifying agent that prevents or reduces effect of anthrax toxin on host cell, for treating human or non-human animal suffering from anthrax.

Claim 7; Page 27-29; 45pp; English.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
787	787	802.2	803.8	803.8	803.8	803.8	819	853.4	853.4	853.4	853.4	867.6	867.6	892.6	912.4	912.4	949	949	949.4	949.4	949.4	949.4	949.4	949.4
71.3	71.3	72.7	72.8	72.8	72.8	72.8	74.2	77.3	77.3	77.3	77.3	78.6	78.6	80.9	82.6	82.6	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0
1436	1436	1718	1609	1609	1609	1402	1534	5220	5220	5220	5220	1623	1623	1608	1047	1047	1008	1008	2353	2272	2272	2272	2112	1713
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ABV73884	AAH14331	ABV30282	ADB48098	ADQ98338	AAI58132	AAI59918	ADI00565	ABX72063	ABX72010	ABL92138	ABL92085	ADM64587	ADI00543	ADI00567	ADM64579	ADI00553	ADM64583	ADI00557	ACN88807	ADM64567	ADI00533	AAA47455	ABV73883	ADM64577
Abv73884 Human ant	Aah14331 Human cDN	Abv30282 Human pro	Adb48098 Novel hum	Adq98338 DNA encod	Aai58132 Human pol	Aai59918 Human pol	Adi00565 Human TAN	Abx72063 DNA encod	Abx72010 DNA encod	Ab192138 Mouse Tum	Ab192085 Mouse Tum	Adm64587 TANGO197	Adi00543 Human TAN	Adi00567 Human TAN	Adm64579 Human TAN	Adi00553 Human TAN	Adm64583 Human TAN	Adi00557 Human TAN	Acn88807 Breast ca	Adm64567 Human von	Adi00533 Human TAN	Aaa47455 Human TAN	Abv73883 Human ant	Adm64577 Human TAN

ALIGNMENTS

RESULT 1 ABV73881 Key CDS WPI; 2002-713235/77. P-PSDB; ABP54903. mat_peptide 05-DEC-2000; 2000US-0251481P. 03-OCT-2001; 2001WO-US030941 WO200246228-A2 sig_peptide Homo sapiens. Anthrax; toxin; receptor; human; antibacterial; gene; ss. Human anthrax toxin receptor cDNA. 08-JAN-2003 (first entry) ABV73881; ABV73881 standard; cDNA; 1414 BP. Young JAT, Bradley KA, (WISC) WISCONSIN ALUMNI RES FOUND. 13-JUN-2002. /*tag= b 183. .1207 /*tag= c /*tag= a /product= "anthrax toxin receptor" 104. .182 Location/Qualifiers Collier RJ, Mogridge JS;

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The present sequence is that of cDNA encoding a human surface-bound CC anthrax toxin receptor (ATR). The cDNA is a PCR amplification product from HeLa cells and human placenta cDNA libraries. Anthrax toxin CC protective antigen (PA) binds to the ATR at a von Willebrand factor A CC domain located in the extracellular domain of ATR. The invention provides ATR polypeptides and polymucleotides, vectors, host cells, and transgenic CC and knock-out animals. The invention also provides methods for centrifying molecules that bind the ATR and which reduce the toxicity of CC involves administering an agent that inhibits binding between PA and ATR CC include ATR or a PA-binding fragment of ATR, a PA-binding polypeptide at CC least 80% identical to these, a fusion protein, a monoclonal or CC least 80% identical to these, a fusion protein, a monoclonal or CC polyplonal antibody, a polypaccharide, a lipid or a monocloca acid. ATR CC polyplonal antibody, a polypaccharide, a lipid or a mucleic acid. ATR CC polypoptides, and as molecular probes
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11-AUG-2000;
11-APR-2001;
The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain tumour endothelial marker (TEM) protein selected from ABB90732, ABB9 ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activit
                                                                                                                                                                                                                                                                                                                                                                                            Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                                  An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                                         Disclosure; Page 121-123;
                                                                                                                                                      WPI; 2002-291856/33.
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              TGTCCAGCGCCTATCTTAAAAGAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC
                                                                                             GTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAG
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11-AUG-2000;
11-APR-2001;
                        The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psoriasis; gene; ss.
endothelial markers (TEM) endothelial markers (NEM) (PEM) ABL91903-ABL91995
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The present sequence is that of cDNA encoding a human anthrax toxin creceptor (ATR). The cDNA, previously designated TEMB, was originally consolated by PCR from HeLa cell and human placenta cDNA libraries. It was cidentified in a database screening using a newly isolated human cDNA (see ABV73881) which encodes an ATR (see ABP54903) that is identical to the CR TEMB polypeptide except in the cytoplasmic tail, suggesting differential constraint of a primary mRNA transcript. TEMB was not previously identified constraint of a primary mRNA transcript. TEMB was not previously identified constraint of the ATR and which constraints and transgenic and knock-out animals. It also constraint of the ATR and which constraints in a human or animal involves administering an agent that constraints binding between anthrax toxin protective antigen (PA) and ATR at level effective to reduce the severity of anthrax. Suitable agents include the TEMB polypeptide or a PA-binding fragment of it, a PA-binding consolonal or polyclonal antibody, a polysaccharide, a lipid or a nucleic acid. ATR polynucleotides can also be used in the recombinant production
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                                                                                  TGTCCAGCGCCTATCTTAAAAGAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC
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Query Match Best Local Similarity Matches 1092; Conserv

98.8%;

Score 1090.8; Pred. No. 0;

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Mismatches

ب 10; 0 U;

Indels

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Gaps

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Length 5540; 0 Other;

BP;

1601 A;

1306 C;

1187 G;

1446 T; DB

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RESULT 5
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ID ABX72029
ID ABX72029
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                                                       The present invention relates to a novel method for the isolation of endothelial cells (ECS), and the identification of genes expressed in normal and tumour ECS. Tumour endothelial marker (TEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
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RESULT 7
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The present invention describes a method for detecting a pancreatic CC cancer-associated transcript in a biological sample. The method comprises CC contacting the biological sample with a polynucleotide that selectively CC hybridises to a sequence at least 80% identical to a sequence as shown in any one of Tables 3 to 25 in the specification or having the GenBank Accession Number AF279145. Also described: (1) diagnosing pancreatic CC cancer in a human or animal subject being tested, determining the CC likelihood that a subject having a pancreatic cancer will survive, or CC determining the suitability of a subject having a pancreatic cancer for CC surgical resection therapy; (2) detecting a pancreatic cancer associated polypeptide in a biological sample; (3) determining the likelihood that a CC subject having a pancreatic cancer associated cancer of a therapeutic treatment of pancreatic cancer. A pancreatic cancer associated in CC gene and protein therapy. A pancreatic cancer cancer. A pancreatic cancer associated polypeptide or an antibody that binds to the isolated polypeptide can be used for diagnostic methods are useful for the polynucleotide, an isolated polypeptide or an antibody that binds to the isolated polypeptide can be used for diagnostic methods are useful for the early detection of pancreatic cancer or the prognosing or prognosing pancreatic cancer. The prognostic or cancer or the metastases, and for monitoring the polynucleotide, an isolated can be used in the metastases, and for monitoring the progress of disease such cancer or its metastases, and for monitoring the progress of disease such cancer cancer or its metastases, and for monitoring the progress of disease such cancer cancer cancer cancer. The prognostic cancer c
Sequence
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cytostatic; gene therapy; protein therapy;
tumour endothelial marker 8 precursor; TEM8; gene; ss.
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DB; ADR48216.
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CC protein genes, and AARD1436-AARD1513 represent the proteins they encode. CC protein genes, and AARD1436-AARD1513 represent the proteins they encode. CC AARD1514-AARD1544 represent human secreted protein fragments or variants. CC The genes and their secreted proteins are useful for preventing, treating CC or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the CC pathological conditions can be diagnosed by determining the presence of mutations in CC the new genes. Specific uses are described for each of the 28 genes, cander the tissues in which they are most highly expressed, and include CC developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, cancer the condition of the immune system, AIDS, autoimmune CC diseases (e.g., rheumatoid arthritis), inflammation, allergies, cognitive disorders (e.g., Alzheimer's disease, Parkinson's disease), CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g., cardiovascular disorders, atherosclerosis, cardiovascular disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; fumnume system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Albeimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; gastrointestinal disorder; promancy-related disorder; cell culture; chemotaxis; food additive; gene therapy; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
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30-JUN-2000; 2000US-0215133P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2447
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                                                                                GTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAG
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XX AADO
XX Huma
XW Huma
XW Huma
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               05-NOV-1999; 99US-0163581P
30-JUN-2000; 2000US-0215133P
                                                        01-NOV-2000; 2000WO-US030045
                                                                                                                                                                                                     sig_peptide
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166. .246
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247. .1
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/transl_except= (pos:688. .690, aa:Xaa)
/transl_except= (pos:1123. .1125, aa:Xaa)
/transl_except= (pos:1156. .1158, aa:Xaa)
/transl_except= (pos:1267. .1269, aa:Xaa)
/note= "Xaa_equals any of the twenty natu
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(HUMA-) HUMAN GENOME SCI INC.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The genes and their secreted proteins are useful for preventing, treating CC or smeliorating medical conditions, e.g., by protein or gene therapy.

CC Pathological conditions can be diagnosed by determining the amount of the constitution of the preventing the protein or gene therapy.

CC new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 28 genes, considered the constitution of the constitution of the constitution of the new genes. Specific uses are described for each of the 28 genes, considered the constitution of the constitution of the new genes, cancer, tumours, foetal and developmental abnormalities, considered disorders, diseases of the immune system, AIDS, autoimmune considerative disorders, diseases of the immune system, AIDS, autoimmune considerative disorders, schizophrenia, asthma, skin disorders (e.g., considered disorders, schizophrenia, asthma, skin disorders, consideration, altergies, considerated disorders, and disorders, gastrointestinal disorders, considerated disorders, endocrine disorders, and infections. The pregnancy-related disorders, endocrine disorders, and infections. The consideration of prevent skin aging due to sumburn, to maintain organs to protein can also be used to aid wound healing and epithelial cell consideration also be used to aid wound healing and epithelial cell consideration of the invention can be used in alleviating symptoms associated consideration of the invention can be used in alleviating symptoms associated consideration of the invention can be used in alleviating symptoms associated considerated and the consideration conversed the abundant assay (ELISA). The present semicar environment as a human secreted protein-encoding conversation conversations.
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 1090;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode AAE01514-AAE01544 represent human secreted protein fragments or variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
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XX Plasm
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fusion; von Willebrand factor A-like domain; vWF; antibacterial;
cutaneous; inhalation anthrax; human; TANGO 197 Ig fusion; mutan
                                                                                                           Human TANGO
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Homo sapiens
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                                                                                                           DNA - plasmid p0610
                                                    Ig fusion; mutant;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 Ig mutated fusion DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor h-lik domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWF.
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DB; ADI00550.
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O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
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                                                 TCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTGTTTACTGTGTTGGTGTG
                                                                                                                                                                                            CANATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG
AAAGATTTCAATGAGACACAGCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTCCC
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0; Mismatches 2;
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New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF.

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Synthetic.
                                                                                                                                                                                                                                                      (ROTT/)
(OKEE/)
(OZKA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; mouse; TANGO197; immunoglobulin; Ig; fusion protein;
                                                                                                                                                                                   Rottman JB,
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                                                                                                                2003-829643/77.
DB; ADM64576.
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OZKAYNAK E.
HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGACACTTATTTACTG
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99.8%;
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Pred. No. 3.9e-284;
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ATGGCCACGGCGAGCGGAGAGCCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT

Query Match Best Local Matches

Similarity

86.3%; 99.4%;

Score 952.4; Pred. No. 1.5e 0; Mismatches

DB 10;

Indels

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Gaps

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Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROTT/) ROTTMAN J B.
(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                 The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 Ig FCR mutated fusion DNA of the invention.
                                                                                                                                                                                                                                                                                                               New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2002; 2002US-00201292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion; von Willebrand factor A-like domain; vWF; antibacterial;
cutaneous; inhalation anthrax; human; TANGO 197 Ig FcR fusion; mutant;
plasmid pLKTOK127; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TANGO
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Sequence
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BP; 427 A; 454 C;
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419 G; 350 T; 0 U; 0 Other;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel fusion polypeptide comprising a von willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or amellorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 Ig FCR wild-type fusion DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or amellorating symptoms of anthrax comprises a von Willebrand factor A-like domain (VWF) amino acid sequence and an amino acid sequence heterologous to the VWF.
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(OKEE/)
(OZKA/)
(HEAL/)
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cutaneous; inhalation anthrax; human; TANGO 197 Ig FCR fusion; wild-type;
plasmid pLKTOK129; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; SEQ ID NO 15;
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O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
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CAPATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG
                CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGGAGACACTTACATG
                                               TCCTTTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTGACAGAAGACAGAGAA
                                                                TCCTTTATTGTTTTCTCCACCCGAGGAAACCAACCTTAATGAAACTGACAGAAGACAGAGAA
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ilarity 99.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion DNA -
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0; Mismatches
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von Willebrand
vWF amino acid
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Synthetic.
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                                                                                                                                                                                                                                                                                                           fragment of crystallisation;
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                                                                                                                                                                                                                                                                                                                                antibacterial; gene therapy;
von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous
inhalation anthrax; human; TANGO197; immunoglobulin G; IgG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This sequence encodes a fusion protein comprising human TANGO197 extracellular region, minus the DG residues closest to the transmembrane region, and immunoglobulin G (IgG) fragment of crystallisation (Fc) with mutations L235A and G237A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (WF) amino acid sequence and an amino acid sequence heterologous
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O'KEEFE T
OZKAYNAK
HEALEY J
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          antibacterial; gene therapy; von Willebrand factor A-like domain amino acid sequence; vWF amino acid sequence; anthrax; Bacillus anthracis; cuinhalation_anthrax; human; TANGO197; immunoglobulin G; I(
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                                     TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or liorating symptoms of anthrax comprises a von Willebrand factor A-like ain (vWF) amino acid sequence and an amino acid sequence heterologous
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                                                                                                                                                                                                                              ROTTMAN J B.
O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
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PS Example; SEQ ID NO 15; 64pp; English.
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The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This sequence encodes a fusion protein comprising human TANGO197 extracellular region, minus the DG residues closest to the transmembrane region, and immunoglobulin G (IgG) fragment of crystallisation (Fc).

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Sequence 1650 BP; 427 A; 453 C; 419 G; 351 T; 0 U; 0 Other;
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                                                                                                ATCGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTCATTTCAAGTTGTC
                                                                                                                                                GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAAGTCCTGC
                                                                                                                                                                                                AAAGATTTCAATGAGACACAGCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTCCC
                                                                                                                                                                                                                                                     TCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTGTTTACTGTGTTGGTGTG
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 ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGACACTTATTTACTG
                                         GTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAG
                                                                                                                                 GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAAGTCCTGC
                                                                                                                                                                                    AAAGATTTCAATGAGACACAGCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTCCC
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Pred. No. 1.5
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Db 781 ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGAATACTTAATTACTG 840 Qy 841 TGTCCAGCGCCTATCTTAAAAGAAGTTGGCATGAAAGCTCCAGGTCAGCATGAAC 900 Bb 841 TGTCCAGCGCCTATCTTAAAAGAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC 900 Qy 901 GATGGCCTCTCTTTAATAAAGAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC Db 901 GATGGCCTCTCTTTATCTCCAGGTTCATCATCACCACACACTGTTCTGACGGT 960 Qy 961 TC 962 Db 961 TC 962 Search completed: June 14, 2005, 14:06:24 Job time: 704 Becs

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1: /cgn2_6/pccdata/1/ina/5A_COMB.seq:*

2: /cgn2_6/pccdata/1/ina/5B_COMB.seq:*

3: /cgn2_6/pcdata/1/ina/6A_COMB.seq:*

4: /cgn2_6/pcdata/1/ina/6B_COMB.seq:*

5: /cgn2_6/pcdata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
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US-08-232-463-14
US-09-806-708B-22
US-09-949-016-16291
US-09-949-016-16291
US-09-298-568-1
US-09-949-233-1
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US-08-728-323A-1
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US-09-298-569-20
US-09-395-693-20
US-09-395-368
US-09-395-368
US-09-390-316-12557
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US-09-148-545-131
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Sequence 8, Appli
Sequence 250, App
Sequence 297, App
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 22, Appl
Sequence 1, Appli
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Sequence 1, Appli
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 21, Appli
Sequence 20, Appl
Sequence 21, Appli
Sequence 21, Appli
Sequence 368, Appl
Sequence 1, Appli
Sequence 12557, Ap
Sequence 1035, Ap
Sequence 1035, Ap
Sequence 1031, Appl
Sequence 1031, Appl
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Sequence 25, Appl	e 25,	Sequence 1, Appli	Sequence 2968, Ap	Sequence 3, Appli	Sequence 13, Appl	Sequence 13, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli								

ALIGNMENTS

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ORGANISM: Homo sapiens FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (309)...(1202)
US-09-620-312D-8
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APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Unn Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Reiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Jou, Ping
APPL
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GENERAL INFORMATION:
                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 805; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: pt_FL_genes Version SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                         ATGGCCACGGCGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT
     ATGGCCACGGCGAGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT
                                                                                                                                                                                                Conservative
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Pred. No. 3.1e-254;
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                                                                                                                                                                                                                                                                                                                Sequence 250, Application Patent No. 6783969 GENERAL INFORMATION: APPLICANT: Tang, Y. Tom
  APPLICANT: 1
APPLICANT: APPLICANT
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zhou, ping
goodrich, Ryle
Asundi, Vinod
Ren, Feiyan
Zhang, Jie
Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunqing
Yamazaki, Victoria
Chen, Rui-hong
Wang, Jianrui
Yang, Jonrui
Yang, Yonghong
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APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Ac
TITLE OF INVENTION: No. 6783969el Nucleic Ac
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt FL genes Version 2.0
LENGTH: 3981
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; LOCATION: (29:
US-09-799-451-250
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Best Local Similarity
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (297)..(1118)
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Pred. No. 3.6e-159;
0; Mismatches 2;
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US-09-774-528-297
; Sequence 297, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Thou, Ping
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhao, Qing A.
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; TYPE: DNA
; ORGANIEM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(1434)
US-09-774-528-297
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APPLICANT: Xue, Aldong J.
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Dunrui
APPLICANT: Drmanae, Radoje T.
APPLICANT: Drmanae, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic Ac
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
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CURRENT FILING DATE: 2001-01-30
NUMBER OF SQ ID NOS: 441
SOFTWARE: pt_FL_genes Version 2.0
SBQ ID NO 297
LENGTH: 1492
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Best Local Similarity
Matches 546; Conserv
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TAAGTGTACAGCTTAATTCTATGCTTTGTCCTGCACCTATCCTGAATAAAGCTGGAGAAA
                       TTTCTGTGGAAGACACTTATTTACTGTGTCCAGCGCCTATCTTAAAAGAAGTTGGCATGA
                                                                                ATGGCAGTGTTCTCTGCACTTACACTGTAAATGAAACATATACAACGAGTGTAAAACCAG
                                                                                                                    TGGAÇAGGGTCCTCTGCAGCTTCAAGATCAATGACTCGGTCACACTCAATGAGAAGCCCT
                                                                                                                                                               GTGTGGGGGAGGAATTTCAGATTGTCTTAAGTGGAAGAGGATTCATGCTGGGCAGTCGGA
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59.2%;
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; Sequence 14, Application US/082; Patent No. 5670367;
; GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
                                                                       TOPOLOGY: linear; IMMEDIATE SOURCE: CLONE: pTZgpt-F1s
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 Matches
                    Query Match
Best Local (
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: EP 91 114
PILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: RE NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1800 Dia
CITY: Alexandria
STATE: VA
                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                         TELEPHONE: (703) 683-4109
                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                    Similarity
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4.3%; Score 47; DB 1; Length 721 ilarity 6.7%; Pred. No. 0.00078; Conservative 199; Mismatches 164; Indels
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US-08-232-463-14/c

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; ORGANISM: Homo sapiens
US-09-621-976-8976
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US-09-621-976-8976/c
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LENGTH: 399
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                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENEST: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
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                                                                        104 RYRRYWYYAKRAKWSKRCTWSTTCYCMKYMAKKCWSYWWSMSMMKWGKSMWWKWTYYYYY
                                                                                                            186 CTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATGTCCTT 245
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                                                                                                                                                                                                                                                                                                                                                                                h 3.8%; Score 42.4; DB 4; Length 399;
Similarity 8.9%; Pred. No. 0.0031;
25; Conservative 142; Mismatches 113; Indels
YMMKWSKMTYWSMMSCYARKCWRTYAKTYTWMTCMTWGKR 5
                                  TATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTG 285
                                                                                                                                                   RKWTRWTYYYYKSYMSMKKTWRMKTAYYWTKRWKMTRTKWTWCTMCWKCTTYWMAGTMMY
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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                               CTCGAGATCTTGGTGCAATTGTTTACTGTGTTGGTGTGAAAGATTTCAATGAGACACAGC 562
                                                                                                   TGACTGATGGAGAACTCCATGAAGATCTCTTTTTCTATTCAGAGAGGGGAGGCTAATAGGT 502
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1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                 3.8%; Score 41.4; DB 1; Length 7218; ilarity 6.8%; Pred. No. 0.055; Conservative 198; Mismatches 174; Indels 0
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FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAEl promoters
US-09-806-708B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-09-806-708B-22
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LENGTH: 1141
TYPE: DNA
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: The University of British Columbia TITLE OF INVENTION: Regulation of Embryonic TY EILE REPERENCE: 4010-59741 CURRENT APPLICATION NUMBER: US/09/806,708B CURRENT FILING DATE: 2001-04-03 PRIOR APPLICATION NUMBER: US 60/147,133 PRIOR FILING DATE: 1999-08-04 NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                       584 AGGATCATGTGTTTCCCGTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 DDKRTRWWKKNNNATGWDDDTKYHMWNNNGCBTVTWMVRYKTDRDWSBKRMNYGMBWWK 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68;
        TCCTCTGCAGCTTCAAGATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGG
                                            NYARABHYGYKWNTRWWBWSHTWBHBRAGAAHYWMBWMYBAKCHCMKAWYKAKKYAGAGG
                                                                                  AGTCATTTCAAGTTGTCGTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACAGGG
                                                                                                                        WDYWWKACTWYKYBVCSKWNNYAAWYTKSSWNYTSRYYRWKTNNSWRWRSDTRSMGRAN
                                                                                                                                                           TTTTGAAGAAGTCCTGCATCGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAG
                                                                                                                                                                                                     RAWDHKTCTHNNTTWWKMKTYWNNCYWKSMTNGKSHRBAAAVYTWYMWWWRRYAHANNNN
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Conservative
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9.8%; Pred. No. 0.026;
lve 270; Mismatches
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GENERAL INFORMATION:

APPLICANT: The University of British Columbia

FITLE OF INVENTION: Regulation of Embryonic Tran

FILE REFERENCE: 4810-58741

CURRENT APPLICATION NUMBER: US/09/806,708B

CURRENT FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: US 60/147,133

PRIOR FILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin version 3.0

SEQ ID NO 22
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; Sequence 22, Application US/09806708B
; Patent No. 6784342
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Best Local
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ORGANISM: Human
FEATURE:
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US-09-949-016-16291/c
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SOFTWARE: FastSEQ for
SEQ ID NO 16291
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APPLICANT: VENTER, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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PRIOR APPLICATION NUMBER: 60/231,498
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                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (1)...(37822)
OTHER INFORMATION: n = A,T,C
                                  Similarity
                                                                                                                                              AAGACACTTATTTACTGTGTCCAGCGCCTATCTTAAAAGAAGTTGGCATGAAAGCTGCAC 883
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                                                                        CAAGAAACCCAGGTAGGGGAAAGAATCTGAGTTTCTAGAATAGACACATTATTTTAAATG
                                                                                                                                                                                  ACCCGAGGAACAACCTTAATGAAACTGACAGAGAACAGAGAACAAATCCGTCAAGGCCTA
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Pred. No. 0.54;
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S OF DETECTION
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FEATURE:
NAME/KEY: promoter
LOCATION: (1)...(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1141
TYPE: DNA
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213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 GGAGACACTTACATGCATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 3.4%; Score 37.6; DB Similarity 10.9%; Pred. No. 0.26;
                                     CCACCCCTGCCGAGGAGAGTGAGGAAAATAAAATAAAA 1104
                                                                                                               crescreterecresiserrerescenterecreterescreterescreterescenterescer
                                                                                                                                                          HMNTHCTYGNNTWGSAYBMAAMSMWAAGASNBVTYNWCWRMTYMGKTMTNNNNNNKAWYY
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                                                                                                                                                                                                                                                                           CAGGTCAGCATGAACGATGGCCTCTCTTTATCTCCAGTTCTGTCATCATCACCACCACA
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  KCRNKYMVSWHYHAMRYBKWABAVGCNNNWKDRMAHHHW 175
                                                                              RTKTVAWCNNRYYYDTAVWTBKRNYKYCYAYBWYYBMYMGKHHWBWWRRABHRSWNMWWV
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RESULT 10 US-08-728-323A-1/c ; Sequence 1, Application

US/08728323A

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Sequence 1, Application US/09298568 Patent No. 6327792 GRMERAL INFORMATION: APPLICANT: Kieff, Elliott D.

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; TELEPAX: 212-391-000 1:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear (genomic)
RESULT 11
US-09-298-568-1/c
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ANAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELESPIONE: 212-78-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/728,323A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEB: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1185 Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP:
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                                                                                                        1063 CCT 1065
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                                                                       969 CTT
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milarity 50.3%;
Conservative
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Pred. No. 0.67
0; Mismatches
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RESULT 12
US-09-410-399-1/c
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/ TYPE: DNA
/ ORGANISM: Kaposi's
US-09-410-399-1
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/ ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1
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SOFTWARE: PatentIn Ve
SEQ ID NO 1
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Best Local
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CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: to Genomic Host DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: HAADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: HAADINO VIRUS DIA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
CURRENT APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
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                                                                               CTCCTCGTCATCCTCGTCATCCTCCTCGTCATCCTCGTCATCCTCCTCGTCATC 1030
CTCCTCGTCCTCATCTGTCTCCTGCTCCTCATCATCCTTATTGTCATTGTCATC
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ilarity 50.3%;
Conservative
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                                                                                                                                                                                                                                                                   3.48;
                                                                                                                                                                                                                                           Score 37.4; DB Pred. No. 0.67; Mismatches
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Pred. No. 0.67
0; Mismatches
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                                                                                                                                                                                                                                                                                    DB 4;
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RESULT 14
US-08-770-379-20
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; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-894-273-1
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US-09-894-273-1/c
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Patent No. 5849564
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Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09894273 Patent No. 6756203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-1001R
CURRENT APPLICATION NUMBER: US/09/894,273
CURRENT FILING DATE: 2001-66-28
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/109,422
PRIOR FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                         APPLICANT: Edelman, Isidore S.
APPLICANT: MOOTE, Patrick S.
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                      CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                               STREET:
COMPUTER:
                                                                                                                                                       ADDRESSEE:
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                                                                                                                                 E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                  Chang, Yuan
Bohenzky, Roy A.
Russo, James J.
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IBM PC compatible
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RESULT 15
US-08-757-669A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6183751
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Best Local Similarity
Matches 92; Conserv
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APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 391-052 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/757,669A
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
CLASSIFICATION:
ATTORNEY/AGENT INF
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: double
                                    FILING DATE:
                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 10036
                                                                                                                                                                                                                       STATE: New York
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TOPOLOGY: linear
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1185 Avenue of the Americas
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ilarity 50.3%;
Conservative
 INFORMATION:
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ID NO: 20:
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (gen
US-08-757-669A-20
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Matches 92; Conserv
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4518
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                               20968 CTÉCTEGTECTÉCATETGTECTGCTECTECTEATCATECTTATTGTEATTGTEATE 21027
                                                                                                                              20908 CTCCTCGTCATCCTCGTCATCCTCGTCATCCTCGTCATCCTCCTCGTCATC
21028
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CTT 21030
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                                CCT 1065
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20907

20967

Search completed: June 14, 2005, 16:47:10 Job time: 233 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
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Gapop 10.0 , Gapext 1.0
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                / Cgn2_6/ptcdata/2/pubpna/USOB_NEW_PUB.seq:*
/ Cgn2_6/ptcdata/2/pubpna/USOB_PUBCOMB.seq:*
/ Cgn2_6/ptcdata/2/pubpna/USOB_PUBCOMB.seq:*
/ Cgn2_6/ptcdata/2/pubpna/USOB_PUBCOMB.seq:*
/ Cgn2_6/ptcdata/2/pubpna/USOSB_PUBCOMB.seq:*
/ Cgn2_6/ptcdata/2/pubpna/USOSC_PUBCOMB.seq:*
/ Cgn2_6/ptcdata/2/pubpna/USOSC_PUBCOMB.seq:*
/ Cgn2_6/ptcdata/2/pubpna/USOSC_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compus
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/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

7654527	Result
1104 1104 1090.8 1090.8 1090.8 1090.8	Score
100.0 100.0 98.8 98.8 98.8 98.8	Query Match
5540 5540 5540 5540	1
10 10 20 20	DB
17 US-10-133-937-8 17 US-10-159-563-58 10 US-09-918-715-176 10 US-09-918-715-231 15 US-10-101-822-198 20 US-10-474-794-176 20 US-10-474-794-231	ID
Sequence 58, Appl Sequence 58, Appl Sequence 176, App Sequence 231, App Sequence 198, App Sequence 176, App Sequence 231, App	Description

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US-10-047-542-100 US-10-302-172-250	-10-047-542-98	-10-201-292-	-10-201-292-2	-10-201-292-3	-10-357-930-	-10-117-722-	-10-037-270-	-10-201-292-3	-10-474-794-30	-10-474-794-	9-918-715-30	-09-918-715-1	-10-062-674-17	0-201-292-1	-10-038-307-1	-10-201-292-3	-10-201-292-2	-038-	-10-201-292-2	-10-038-307-25	-10-198-846-9	-10-201-292-	-10-038-307-1	-09-796-753-	-10-201-292-1	-10-038-307-1	10-201-292-2	-10-038-307-2	-10-201-292-	-10-038-307-	-10-201-292-1	-10-201-292-	-10-038-307-1	38-307-1	-10-201-292-	-10-038-30/-I
Sequence Sequence	equence	equence	equence	equence	equence	equence	equence	equence	equence	equence	equence	equence	equence	equence	Ø	equence	equence	equence	equence	equence	equence	equence	equence	equence	equence	equence	equence	equence	equence	equence	equenc	equenc	Ò	quenc	Sequence	sequence
100, Ap 250, Ap	φ,		27, App	7	30300, 1	•	-	~	•	•	300, App	186, A	1757,	11, Ap	11, Ap	35, Ap	21, Appl	21, Ap	25, Ap	25, Ap	9957,	1, Appli	1, App	11, Ap	19, Ap	19, Ap	23, Ap	23, Ap	9, App	9, App	•	i.,		13, Ap	- 1	_

ALIGNMENTS

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-133-937-58
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US-10-133-937-58
; Sequence 58, Application US/10133937
; Publication No. US20030207278A1
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                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
                                                                                        Matches 1104; Conservative
                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                               APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
TITLE OF INVENTION: OTHER BIOLOGICAL STATES
FILE REFERENCE: 11613.56US01
CURRENT APPLICATION NUMBER: US/10/133,937
CURRENT FILING DATE: 2002-11-04
144 ATGGCCACGGCGGAGCGGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT 203
                       1 ATGGCCACGGCGGAGAGCCCTCGGCATCCAGTGGCTCTCTTTGGCCACT
                                                                                                      100.0%; Score 1104;
100.0%; Pred. No. 0;
                                                                                        0; Mismatches
                                                                                                                                   DB 17;
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GAGAGTGAGGAAAATAAAATAAAA
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US-10-159-563-58
Sequence 58, Application US/10159563
Publication No. US2004009154A1
GENERAL INFORMATION:
APPLICANT: Khan, Javed
APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: SELECTIONS OF GENES AND
TITLE OF INVENTION: DIAGNOSIS AND FOR TARGE
FILE REFERENCE: 11613-56US11
CURRENT APPLICATION NUMBER: US/10/159,563
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 10/133,937
PRIOR APPLICA
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                                                                   TCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTGTTTACTGTGTTGTTGGTGTTG
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OY 61 CTGGTGCTCATCTGCGCCGGGCAAGGGGAAGGAAGGAAGG	Query Match 98.8%; Score 1090.8; DB 10; Length 5540; Best Local Similarity 99.8%; Pred. No. 0; Matches 1092; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 1 ATGGCCACGGCGGAGGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT 60	Qy 1021 TGGTTCTGGCCCTGTGCTGATCCTGCTCAGCCCTGCCTGC	Oy 661 ATCGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTCATTTCAAGTTGTC 720
RESULT 4 US-09-918-715-231 ; Sequence 231, Application US/09918715 ; Publication No. US20030017157A1 ; GENERAL INFORMATION: ; APPLICANT: Brad St. Croix	Db 1164 TGGTTCTGGCCCTCTGCTGCACTGTGATTATCAAGGAGGTCCCTCCACCCCTGCCGAG 1223 Oy 1081 GAGAGTGAGGAAAA 1094 [Oy 481 TCAGAGAGGGAATATAGGTCTCGAGATTCTTGATGTGTTGTTGTTGTTGTTGTTGTTTGT	Db 264 GGCGGATTTGACCTGTACTTTTGGACAAATCAGGAAGTGTGCCACCACTGGAAT 323 Qy 181 GAAATCTATTACTTTGTGGAACAGTTGGCTCACCACAATTCATCAGCACCACAGTTGAGAATG 240

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APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: BNDOTHELIAL CELL EXPRESSION PAI
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: U9/09/918,715
CURRENT APPLICATION NUMBER: 60/222,599
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity
Matches 1092; Conserv
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LENGTH: 5540
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; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144)...(1838)
US-10-301-822-198
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APPLICANT: Burgart, Lawrence J.

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-02992RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR PILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/361,978
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Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows
SEQ ID NO 198
LENGTH: 5540
                                                                                                                  Query Match
Best Local Similarity
                                                                                                      Matches 1092;
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APPLICANT:
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Schlegel, Robert
Monahan, John E.
                                                                                                      Conservative
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                                                                                                                  Score 1090.8;
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APPLICANT: Vogelstein, Bert
APPLICANT: Vinzler, Kenneth
APPLICANT: Winzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
VINDBER OF SEQ ID NOS: 359
SOPTWARE: PastSEQ for Windows Version 4.0
EENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
US-10-474-794-176
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Best Local Similarity
Matches 1092; Conserv
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Publication No. US20040213793A1
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APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
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                                                                     GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAAGTCCTGC
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APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PAT
FILE REFERENCE: 1107.00179
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-01
NUMBER OF SEQ ID NOS: 359
SOPTWARE: FRSUSCH IN ONE SEQ ID NO 231
LENGTH: 5540
TYPE: DNA
ORGANISM: Homo sapiens
US-10-474-794-231
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Matches 1092
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ilarity 99.8%;
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Pred. No. 0;
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                                                                                           RESULT 8
Sequence 17, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
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APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 1674
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-17
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ATCAATGACTCGGTCACACTCAATGAGAAGCCCTTTTCTGTGGAAGATACTTATTTACTG
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Pred. No. 3.9e-303;
0; Mismatches 2;
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Sequence 17, Application US/10201292

Publication No. US20030144193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEBFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Mudith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT PILING DATE: 2003-02-14

INUMBER OF SEQ ID NO 17

SEQ ID NO 17

LENGTH: 1674

TYPE: DNA

ORGANISM: Homo sapiens

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             TCAGAGAGGGGAGGCTAATAGGTCTCGAGATCTTTGGTGCAATTTGTTTACTGTGTTGGTGTG
                                                                                                                 CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAACAGACAAGGGTACAGG
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                                                                 ACAGCCAGCGTCATCATTGCTTTGACTGATGAGAACTCCATGAAGATCTCTTTTTCTAT
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Pred. No. 3.9e-303;
0; Mismatches 2;
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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: LUdith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Com
FILE REFERENCE: 7853-253-99
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1650
TYPE: DNA
ORGANISM: Homo sapiens
US-10-038-307-13
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Sequence 15, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZZAYNAK
APPLICANT: LOGIN TANGO 197 and Tango 216
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT ELING DATE: 202-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1650
TYPE: DNA
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Pred. No. 2.2e-300;
0; Mismatches 6;
                                          CCAGTTCTGTCATCATCACCACACACACTGTTCTCCCAAA 960
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-13
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US-10-201-292-13
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Hodin OZKAYAAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
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Local Similarity 99.4%;
tes 956; Conservative
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                                          GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAGAAGTCCTGC
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 ATCGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTCATTTCAAGTTGTC
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Pred. No. 2.2e-300;
Pred. No. 6;
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Sequence 15, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CCURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
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; ORGANISM: Homo sapiens
US-10-201-292-15
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US-10-201-292-15
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                                                                                   TCCTTTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTGACAGAGACAGAGAA 300
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Pred. No. 2.2e-300;
0; Mismatches 6;
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US-10-038-307-9
; Sequence 9, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-307-9
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Best Local Similarity
Matches 955; Conserv
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
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                                                         Conservative
                                                                   86.1%;
                                                       Score 950.8; DB 15
Pred. No. 7.3e-300;
0; Mismatches 7;
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RESULT 15
US-10-201-292-9
US-10-201292-9
Sequence 9, Application US/10201292
; Publication No. US20030144193A1
; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE
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                                            GTGAGAGGAAACGGCTTCCCGACATGCCCGCAACGTGGACAGGGTCCTCTGCAGCTTCAAG
                                                                    ATCGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTCATTTCAAGTTGTC
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; APPLICANT: Engin OZKAYNAK
; APPLICANT: Judith J. HEALEY
; TITLE OF INVENTION: Tango 197 and Tango 216
; FILE REFERENCE: 7853-253-999
; CURRENT APPLICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-201-292-9
Score 950.8; DB 15
Pred. No. 7.3e-300;
0; Mismatches 7;
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Search Job tim	Db	Ś	뫄	δ	В	Ş
Search completed: June 14, 2005, 18:37:32 Job time : 786 secs	961 TC 962	961 TC 962	901 GATGGCCTCTCTTTTATCTCCAGTTCTGTCATCATCACCACCACACACTCTTCTCCCCAAA 960	901 GATGGCCTCTCTTTTATCTCCAGTTCTGTCATCATCACCACCACACACA	841 TGTCCAGCGCCTATCTTAAAAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC 900	841 TGTCCAGCGCCTATCTTAAAAGAAGTTGGCATGAAAGCTGCACTCCAGGTCAGCATGAAC 900

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Result
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1957)
1 (bases 1 to 1957)
1 (h.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Peng Liang Email : fliang@lifetech.com URL :
Contact : Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                  1 ATGGCCACGGCGGAGCGGAGAGCCCTCCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT
                                                                                                                                                                                                                                                                                                 division of Invitrogen.
Location/Qualifiers
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-JUL-2004) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope.
Direct Submission
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                                                                             Conservative
                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO35YA13"
/tissue_type="Placenta Cot 2"
/plasmid="pCMVSPORT_6"
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Group Phase I & II Team.
Analysis of the mouse transcriptome based on
of 60,770 full-length cDNAs
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                                                    URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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Please visit our web site for further
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue type="testis"
/clone Tib="RIKEN full-length enriched
/dev stage="13 days embryo"
1. .3161
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MARKER 8) homolog [Mus musculus] (SWISSPROT|Q9CZ52,
evidence: FASTY, 100%ID, 84.6%length, match=1428)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="6030436P19"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="FANTOM_DB:6030436P19"
/db_xref="taxon:10090"
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/strain="C57BL/6J"
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Pred. No. 9.4e-242;
0; Mismatches 136;
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JOURNAL
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Best Local :
                                                                                                                             Matches
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                                                                                                                                              Local Similarity
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5-PRIME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence belongs to sequence cluster 1660.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODEO11CF05QP1&c=1660.f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was not normalized. Library was constructed by Life Technologies, division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
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2 rue Gaston Cremieux, CP 5706 - 91057 EV
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1 (bases 1 to 106)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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AL542724.3 GI:45718299
  CTGGTGCTCATCTGCGCCGGGCAAGGGGACGCAGGGAGGATGGGGGTCCAGCCTGCTAC
                                                                ATGGCCACGGCGAGGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT
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                                                                                                                                                                                                                            /tissue type="PIACENTA"
/clone Tib="Homo sapiens PLACENTA"
/clone Tib="Homo sapiens PLACENTA"
/clone Tib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE011YL09"
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                                                                                                                                            62.4%;
99.0%;
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                                                                                                                        Pred. No. 4.36
1; Mismatches
                                                                                                                                              Score 689.2; DB 1;
Pred. No. 4.3e-193;
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RESULT 4
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AUTHORS
TITLE
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                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11448 row: n column: 07
                                                                                                                                                                                                                                                                                                   mRNA sequence.
BI823853
                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                        BI823853
603039031F1 NIH_MGC_115 Homo
                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                   quality sequence stop: E
Location/Qualifiers
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                         GI:15935416
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Primates;
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sapiens
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              GTCGTGAGAGGGAAACGGGTTTCCGACATGCGCGGCAAACGTGGACCAGGGTCCTCTTGG
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/note=Worgan: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: ECGNV (destroyed); RN source anonymous pool of 6 male brains, age range 23-27; male lung, age 27; and 1 male testis, age 69. Library i oligo-dT primed and directionally cloned (ECGNV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5179974"
/lab_host="DH108"
/clone_lib="NIH_MGC_115"
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/db_xref="taxon:9606"
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1 ATGGCCACGGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT Similarity CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAACAGACAAGGGTACAGG CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGAGACACTTACATG GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATG GGCGGATTTGACCTGTACTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCACTGGAAT CTGGTGCTCATCTGCGCCGGGCAAGGGGAGGAAGGATGGGGGTCCAGCCTGCTAC CATC-GAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTC-ATTTCAAGTT GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTTG-AAGAAGTCCTG AAAGATTTCAATGAGACACAGCTGGCCCCGGATTGCGGACAGTAAGGATCATGTGTTTCCC TCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTGTTTACTGTGTTGGTGTG ACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAACTCCATGAAGATCTCTTTTTCTAT TCCTTTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTGACAGAAGACAGAGAA GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATG ATGGCCACGGCGGAGCGGAGAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT GTCGTGAGAGGG--AAACGGCTTCCGACATGCCCG--CAACGTGGACAGGG---TCCTCTG 770 CATCGGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAGTCAATTCCAAGTT GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATTTTGAAAGAAGTCCTG ACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAACTCCATGAAGATCTCTTTTTCTAT CATGAAGGATTTGAAAGGGCCAGTGAGCAGATTTATTATGAAAACAGACAAGGGTACAGG CAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTACATG TCCTTTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTGACAGAAGACAGAGAA GGCGGATTTGACCTGTACTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCACTGGAAT Conservative 62.0**%**; 95.1**%**; <u>,</u> Score Pred. Mismatches e 684.6; DB 4; . No. 9.4e-192; ismatches 29; Indels Length 878; 11; Gaps 655 600 595 540 536 480 476 420 416 360 356 296 236 180 176 120 116 60 715 775

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                                            L Nature 420, 563-573 (2002)

E 6 (Dases 1 to 1614)

E 8 Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Puruno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Furuno,M., Konda,F., Imotani,K., Ishi,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Kosukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,X., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Yoshino,M., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Physical and Chemical Research (RIKEN), Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium and the
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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GARAGARAGARICCHARAGCITCITTITTITTITTITTITYN 3,], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exploration Research Group, RIKEN Genomic Sciences Center (GSC) RIKEN Yokohama Institute; 1.7-22 Suehiro-cho, Tsurumi-ku, Yokoh Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence [5'
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                                                                                                                                                                                                                                                                                                                                         ACAACCTTAATGAAACTGACAGAAGACAGAGAACAAATCCGTCAAGGCCTAGAAGAACTC 327
CAGAAAGTTCTGCCAGGAGGAGACACTTACATGCACGAAGGATTCGAGAGGGCCAGTGAG
                                                                                                                                                                                                                                CAGAAAGTTCTGCCAGGAGGAGACACTTACATGCATGAAAGGATTTGAAAGGGCCAGTGAG 387
                                                                                                                                                                                                                                                                                                          ACAACTTTAATGAAACTAACTGAGGACAGGGAACAGATCCGACAAGGCCTAGAAGAGCTC 61
                                                                                     CAGATTTACTATGAGAACAGTCAAGGATACAGGACGGCGAGCGTCATCATCGCGTTGACG 181
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ilarity 89.0%;
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GLPKKKWPTVDASYYGGRGVGGIKRMEVRWGEKGSTEEGAKLEKAKNARVKMPEQEYE
FPEPRNLNNNMRRPSSPRKWYSPIKGKLDALWVLLRKGYDRVSVMRPQPGDTRFRGWR
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GYRFASVIIALTDGELHEDLFFYSEREANRSEDLGAIVYCVGYKDFNEFQLARIADS
KDHYFPVNDGFQALGGIIHSILKKSCIEILABAPSTICAGESFQVVVRGMGFRHARNS
KDHYFPVNDGFCALGGIIHSILKFYSEREARRSEDLGAIVYCVGYKDFNFERISSSV
DRVLCSFKINDSVTLNEKPFAVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSV
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/protein_id="BAB28591.1"
/db_xref="GI:12850100"
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10, 11 days embryo"
11. .1306
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                                                    Email: cgapbs remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAM12338 row: j column: 13
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1054)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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AGENCOURT 6420797 NIH_MGC_72

5', mRNA sequence.

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/db_xref="taxon:9606"
/clone="ImAGE:5541228"
/clone="ImAGE:5541228"
/lab_host="DH10B (phage-resistant)"
/clone lib="WIH MGC 72"
/note="Organ: Skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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Pred. No. 5.4e-185;
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http://image.llnl.gov
plate: NDAM1166 row: j column: 11
High quality sequence start: 6
High quality sequence stop: 688.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892
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Mammalia; Eutheria; Primatea; Catarrhini; Hominidae; Homo.
1 (bases 1 to 833)
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C0245219
C0245219.1 GI:49108057
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Tissue Procurement: Mary Hendrix
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                 GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATG 240
                                                                                                                                                                               GGCGGATTTGACCTGTACTTTTGGACAAATCAGGAAGTGTGCTGCACCACTGGAAT 180
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                                                                                                                                                                                                                                                                                                                                         ATGGCCACGGCGGAGCCGCAGCCCTCGGCATCGGCTTCCAGTGGCTCTCTTTGGCCACT 60
                     TCCTTTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTGACAGAGACAGAGAA 300
                                                                          GAAATCTATTACTTTGTGGAACAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATG
                                                                                                                                                  GGCGGATTTGACCTGTACTTCATTTTGGACAAATCAGGAAGTGTGCTGCACCACTGGAAT
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TCCTTTATTGTTTTCTCCACCCGAGGAACAACCTTAATGAAACTGACAGAAGACAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NIH_MGC_212"
/note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
/note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agazone
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/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:30924322"
/tissue_type="Chondrossarcoma Lung Metastasis cell lines"
/lab_host="DH108 (TI phage resistant)"
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Pred. No. 4.4e-184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3948114"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov Plate: LLCM810 row: n column: 19
High quality sequence stop: 711.
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National Institutes of Health, Mammallan
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                    /note="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site_2 EcoRI; cDNA made by oligo-dT priming. DIrectionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                    /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
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                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 963)
                                                                                                                                                                                            mRNA sequence.
BG326444
BG326444.1 GI:13132881
               Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                               Craniata; Vertebrata; Euteleostomi;
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GTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCACTCAATT
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/mol type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:4563020"
/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 14"
/clone lib="NIH MGC 14"
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ECORI; cDNA made by oligo-df priming. Directionally cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Tissue Procurement: ATCC/DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                             CTGGTGCTCATCTGCGCCGGGCAAGGGGGACGCAGGGATGGGGGGTCCAGCCTGCTAC 120
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GAACAAATCCGTCAAGGCCTAGAAGAACTCCAGAAAGTTCTGCCAGGAGGAGACACTTAC
                                                                                                                      GAAATCTATTACTTTGTGGAACAGTTGGGTTCACAATTTCATCAGCCCACAGTTGAAAAT
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/mol type="mRNA"
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/db_xref="taxon:9606"
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/clone lib="NIH MGC 20"
/clone lib="NIH MGC 20"
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/clone dinto ECORI/Xhol sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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96.1%;
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Pred. No. 2e-161;
0; Mismatches 19;
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CF132432.1
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Pax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
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University of Iowa
375 Newton Road , 4156
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IMAGE:30560079 5', mRNA seguence.
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UI-HF-ET0-AVV-0-15-0-UI.r1 NIH_MGC_214 Homo
IMAGE:30560510 5', mRNA sequence.
CF126791
CF126791.1 GI:33204381
EST.
услоте Res. 6 (9),
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                                                 1 (bases 1 to 780)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two appr
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                     discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with Oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GATAAGGCCA. Tissue was provided by Mary Hendrix."
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Pred. No. 2.4e-152;
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Tissue Procurement: Mary Hendrix
CDNA Library preparation: Dr. M. Bento Soares, University of cDNA Library Arrayed by: Dr. M. Bento Soares, University of J DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfl.html
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375 Newton Road, 4156 MEBRF, Iowa City,
Tel: 319 335 8250
Pax: 319 335 9565
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ACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAACTCCATGAAGATCTCTTTTTCTAT 480
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/lab host="PH108 (TI phage resistant)"
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Pred. No. 3.6e-149;
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., B Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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Phasianinae; Gallus.
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/notes Torgan: trunks; Vector: pBluescript II KS(+);
Site 1: ECORI; Site 2: Not1; Modification of pBluescript
II KS(+) [Stratagene] vector to accommodate cDNA produced
with the T-trimmed protocol (Construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
NotI and ECORI. Ligate in double stranded adaptor
containing BegI and BamHI sites
[5'ggccgcgtgcagcccggatccggaaaaaaaag]
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/strain="White Leghorn,
/db_xref="taxon:9031"
/clone="ChEST73e23"
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/lab_host="DH10B"
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                                                                                                                                   Unpublished (2003)
Contact: Speleman, F.
Center for Medical Genetics
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92b4 INR32 SSH Homo Bapiens
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 564)
De Preter,K., Pattyn,F., Berx,G., Menten,B., Van Roy
Paepe,A., Speleman,F. and Vandesompele,J.
                                              Tel: 3292402451
Fax: 3292404970
                                                                                       Ghent University Hospital
De Pintelaan 185, 1K5, 9000 Ghent,
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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                        franki.speleman@UGent.be
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1 (bases 1 to 877)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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clone CSODI035YA13 5-PRIME, mRNA sequence.
BX364961
                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                         Homo sapiens
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                                                                                     sapiens (human)
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/mol type="mRNA"
/db xref="taxon:9606"
/cell type="Neuroblastoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="IMR32_SSH"
/note="Vector: pGEM-T Easy; PCR select -
subtractive hybridisation (SSH)"
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Pred. No. 7.7e-147;
0; Mismatches 18;
                                                                                                                                                                                                                                             978
                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local Similarity
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - France
Email: segref@genoscope.cns.fr
Email: segref@genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS1AI009ZE07QP1&c=1660.f. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGTTGGCTCACAAATTCATCAGCCCACAGTTGAGAATGTCCTTTATTGTTTTCTCCACC
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                                                                                                                                             GCTGGCCCGGATTGCGGACAGTAAGGATCATGTGTTTCCCGTGAATGACGGCTTTCAGGC
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                               TCTGCAAGGCATCATCCACTCAATTTTGAAGAAGTCCTGCATC
                                                                                                                                                                                                              TCTCSAGATCTTGGTGCAAWTRTTTACTGTGTTKGGTGTKAAAGATTTCAATGAGACACA
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone="Ist strand cDNA was primed with a NotI-oligo(dT)
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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Pred. No. 3.6e-146;
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US-08-362-652-46
US-08-485-618-46
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US-09-688-307A-46
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Query Match 10.8%; Score 166; DB 1; I Best Local Similarity 28.2%; Pred. No. 6.9e-09; Matches 66; Conservative 42; Mismatches 96;

Length 1155; Indels 30;

Gaps

83

11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK

FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATE: PRIOR PEPLICATION UNMERR: US 08/173,497 PILING DATE: 23-DEC-1993 ATTORNEY/AGENT INFORMATION: NAME: Williams Jr., JOSSEPh A. REGISTRATION NUMBER: 238,659 REFERENCE/DOCKET NUMBER: 27866/32168 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300	W. Mich 'ieren, Mon No. 547095 51 S: O'Toole Wacker Dri ates M: Ates PC-DOS/MS- Release # ATA:	28 159.5 10.4 1161 1 US-08-362-652-55 Sequence 55, A 30 159.5 10.4 1161 2 US-08-605-672-55 Sequence 55, A 31 159.5 10.4 1161 2 US-08-68-933-555 Sequence 55, A 32 159.5 10.4 1161 3 US-09-193-043-55 Sequence 55, A 32 159.5 10.4 1161 4 US-09-688-307A-55 Sequence 55, A 34 159.5 10.4 1161 4 US-09-688-307A-55 Sequence 55, A 35 156 10.2 1161 1 US-08-173-497-2 Sequence 27, Ap 36 156 10.2 1161 1 US-08-173-497-2 Sequence 27, Ap 37 156 10.2 1161 1 US-08-485-618-9 Sequence 27, Ap 38 156 10.2 1161 1 US-08-485-618-9 Sequence 29, Ap 39 156 10.2 1161 1 US-08-485-618-9 Sequence 29, Ap 39 156 10.2 1161 1 US-08-485-618-9 Sequence 29, Ap 39 156 10.2 1161 2 US-08-605-672-2 Sequence 29, Ap 39 156 10.2 1161 2 US-08-605-672-2 Sequence 29, Ap 39 156 10.2 1161 2 US-08-605-672-9 Sequence 29, Ap 39 156 10.2 1161 2 US-08-605-672-9 Sequence 29, Ap 30 156 10.2 1161 2 US-08-605-672-9 Sequence 29, Ap 30 156 10.2 1161 2 US-08-605-672-9 Sequence 29, Ap 30 156 10.2 1161 2 US-08-605-672-9 Sequence 29, Ap 30 156 10.2 1161 2 US-08-482-293A-2 Sequence 29, Ap 30 156 10.2 1161 2 US-08-482-293A-2 Sequence 29, Ap 30 156 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9 Sequence 29, Ap 31 159 10.2 1161 2 US-08-943-363-9
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FILING DATE: 21-DEC-17.
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 27866/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 132-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 46, Application US/08485618 Patent No. 5728533
                                                                              Matches
                                                                                                                    Query Match
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 5-AUG-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                      TENGTH: 1155
TYPE: amino acid
                                                                                                   Local
                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                   11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
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                                                                                                   Similarity
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PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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233 South Wacker Drive, 6300 Sear Tower
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                                                                                Conservative
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                                                                         10.8%; Score 166; DB 1; Length 1155;
28.2%; Pred. No. 6.9e-09;
Live 42; Mismatches 96; Indels 3
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US-08-362-652-46
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Patent No. 57boo...
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
APPLICANT: No. 5766850el Human
TOTO OF INVENTION: No. 5766850el Human
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PRIOR APPLICATION NAMBER: US 08/286,8
PILING DATE: 5-AUG-1994
PILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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1es 66; Conservative
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                                    204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
                                                                                                                    144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                           LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL
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233 South Wacker Drive, 6300 Sear Tower
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Pred. No. 6.9e-09;
2; Mismatches 96
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US-08-605-672-46
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Best Local Similarity
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PRIOR APPLICATION DATA: US 08/286,889
APPLICATION UNMBER: US 08/286,889
PILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PATENTIN Release #1.0, Ve. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
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INFORMATION FOR SEQ ID NO:
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LENGTH: 1155 amino acids
TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 2786
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CITY: Chicago
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                                                                                                                                                               11 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
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                               TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                                                       LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
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TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF 315
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28.2%; Pred. No. 6.9e-09;
tive 42; Mismatches 96;
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US-08-482-293A-46
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
APPLICATION NUMBER: US 08/286,889
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM CO-DOS/MS-DOS
OFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
Marshall, O'Toole, Gerstein, Murray & Borun
ADDRESSEE: Marshall, O'Toole, G300 Sear Tower
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                         204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
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                                             TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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                                                                                         TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
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RESULT 6
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Best Local Similarity
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APPLICATION NUMBER: US 08/173,497

PILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

PILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

PILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,559

REFERENCE/DOCKET NUMBER: 27866/32684
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APPLICANT: Gallatin, W. MICHAEL
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha
TITLE OF INVENTION: 114
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 1155 amino aci
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TELEFAX: 25-3856
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                                 174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                       123 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                                                                                            204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                  144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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                                                                                                                                                                              69 LTEDR----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIJAL 122
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KVGN-FVALRSIQRQIQEK---
                                                                       TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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 IFAIEGTESRSSSSFQHEMSQEGFSSALSMD
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RESULT 8
US-09-688-307A-46
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                                                 PRIOR FILING DATE: 1996-02-22
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-12-21
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION UNMERE: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
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SEQ ID NO 46
LENGTH: 1155
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Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
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Best Local Similarity
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EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
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CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/605,672
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APPLICATION NUMBER: 08/943,363 FILING DATE: 1997-10-03
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 46
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
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EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1998-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 6620915el Human 2
FILE REFERENCE: 27866/35004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 08/362,652 EARLIER FILING DATE: 1994-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1997-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 08/943,363
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1155
TYPE: PRT
ORGANISM: Mus musculus
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Local Similarity 28.2%;
                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                          144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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                                           TDGELHEDLFFYSB--REANRSRDLGAIVYCVGVKD-FNB-TQLARI-----ADSKDHVF 173
                                                                                       FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSFQHEMSQEGFSSALSMD 364
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TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                               Score 166; DB 4; Length 1155;
Pred. No. 6.9e-09;
42; Mismatches 96; Indels 3
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Pred. No. 6.9e-09;
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US-08-485-618-53
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 1161 amino ac
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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APPLICATION NUMBER: US 08/173,497
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CLASSIFICATION:
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CITY: Chicago
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o. 572853
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                                                                                                                                                            69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122
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PVNDGFQALQGIIHSILKKSCIEILAABPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                               TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                                                                                                                                                                                              PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 68
                                        TDGQKFRDPLEYRHVIPEAEKA----GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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233 South Wacker Drive, 6300 Sear Tower
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                                                                                                                                                                                                                                                                                     Score 166; DB 1;
Pred. No. 6.9e-09;
2; Mismatches 96
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RESULT 11
US-08-362-652-53
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                                                                                                                                                                                                                                                                                            Matches
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Best Local :
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1161 amino
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prote
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FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
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APPLICATION NUMBER: US 0
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Van der Vieren,
TITLE OF INVENTION: NO. 57
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TELEPHONE: 312-474-0448
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                                174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVVRGNGFRHARNVD 227
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                                                                                                          123 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 173
                                                                                                                                            204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                    144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                              69 LTEDR-----EQIROGLEELOKVLPGGDTYMHEGFERASEQIYYENROGYRTA-SVIIAL 122
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KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD
                                                                      TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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                                                                                                                                                                                                                                                                                                         Score 166; DB 1;
Pred. No. 6.9e-09;
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RESULT 12

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RESULT 13
US-08-482-293A-53
· Sequence 53, Application US/08482293A
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PRIOR APPLICATION UMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino aci
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REFERENCE/DOCKET NUMBER: 276
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/362
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
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CLASSIFICATION: 530
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STATE: Illinoi
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                                                                                                                                   316
                                                                                                                                                                        174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
                                                                                                                                                                                                                                                                                           204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                                                                      144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                                                                                                                                                                               69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL
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                                                                                                                                   KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                                                                 TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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233 South Wacker Drive, 6300 Sear Tower
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RESULT 14
US-08-943-363-53
US-08-943-363-53
Sequence 53, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
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US-08-482-293A-53
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Best Local Similarity
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
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APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 5831029el Human
TITLE OF TANTONCES: 103
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LENGTH: 1161 amino
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION US/08/440
FILING DATE:
CLASSIET
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ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
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MEDIUM TYPE: Floppy disk
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CITY: Chicago
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INFORMATION:
CANT: Gallatin, W. Michael
CANT: Gallatin, W. Michael
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                                                                                                                                          KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSFQHEMSQEGFSSALSMD
                                                                                                                                                                                                              TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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RESULT 15
US-09-193-043-53
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Sequence 53, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, michael W.
APPLICANT: Van der Vieren, Monica
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human
NUMBER OF SEQUENCES: 114
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APPLICATION NUMBER: US
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TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 27
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                                                                                                                                                                                                                                                                                                                                   FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
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                                                                                                                                                                                                                                                     TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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Pred. No. 6.9e-09;
2; Mismatches 96;
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FILLER APPLICATION NOMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIA DATE: 1997-10-03
INUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIA DATE: 1997-10-03
INUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIA VET. 2.0
SEQ ID NO 53
LENGTH: 1161
TYPE: PAT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.8%; Score 166; DB 3; Length 1161; Best Local Similarity 28.2%; Pred. No. 6.9e-09; Matches 66; Conservative 42; Mismatches 96; Indels 3:
316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSFQHEMSQEGFSSALSMD 364
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                                                                     174 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 227
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Search completed: June 13, 2005, 20:05:07 Job time : 29.681 secs ફ 밁 8 8 8 8 ঠ 69 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 122

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Database
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
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DB seq length: 2000000000
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                                                                                                                                    US-09-970-076-2_COPY_27_321
1536
                                                                                   18:
19:
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_
/ Ggn2_6/ptodata/1/pubpaa/USOB_NEW_PUB_pep:*
/ Ggn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/USO9_NEW_PUB_pep:*
/ Ggn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
/ Ggn2_6/ptodata/1/pubpaa/USOE_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUS-NEW_PUB.pep:*
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1195.537 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

110 0 0 0 5 4 3 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Regult No.
1536 1536 1536 1536 1536 1536 1532 1532 1532 1532 1532 1532 1532 1532	Score
100.0 100.0 100.0 100.0 100.0 100.0 99.7 99.7	Query
3 3 3 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	
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US-09-918-715-187 US-09-918-715-232 US-09-918-715-232 US-10-301-022-199 US-10-408-765A-1823 US-10-474-794-187 US-10-474-794-232 US-10-474-794-232 US-10-038-307-18 US-10-201-292-18 US-10-201-292-18 US-09-833-245-620 US-09-833-245-620	SUMMARIES
Sequence 187, App Sequence 232, App Sequence 199, App Sequence 1893, App Sequence 187, App Sequence 232, App Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 620, App Sequence 12, Appl	Description

44	4.4	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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587	488	488	488	488	538	460	460	479	504	529	534	534	543	543	543	543	543	543	342	342	328	328	562	562	562	562	564	564	345	345	333	333
9 15	14	14	14	10	13	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	16	16	10	10	14	14	14	14	14	14
US-10-104-047-2639 US-09-764-870-312		-10-201-292-	•	53-	-10-047-	US-10-201-292-30	US-10-201-292-28	-292-	-292-	-10-201-292-3	US-10-201-292-12	-10-038-307-1		-307-	-10-201-292-	-10-201-292-	-10-038	-10-038-307-	US-10-201-292-22		-201-	-038-307-	US-10-474-794-301	-794-1	L	US-09-918-715-194	-201-292-	US-10-038-307-20	US-10-201-292-24	US-10-038-307-24	- 1	US-10-038-307-2
Sequence 2639, Ap Sequence 312, App	16, A	е 6,	δ,	e 52,	e 99,	30,	28,	e 32,	34,	36,	12,	12,	e 10,	e 10,	16,	14,	16,	14,	22,	22,	26,	e 26, 1	e 301,	O	e 301,	e 194,	e 20,	æ	e 24,	Sequence 24, Appl	e 2,	Sequence 2, Appli

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR PILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR PILING DATE: 2000-12-21
PRIOR PILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER: OF SEQ ID NOS: 2267
SOPTWARE: PATENTIN VET: 2.1
SEQ ID NO 621
LENGTH: 403
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                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo mapiens
US-09-833-245-621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 621, Application US/09833245 Publication No. US20040010134A1 GENERAL INFORMATION:
                                                                                                                                                                Query Match
Best Local
                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PF546PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Human Genome Sciences, Inc. TITLE OF INVENTION: Albumin Fusion Proteins
                                                                                                                                                                Local Similarity
                                                                                                                                           295;
61 TRGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVII
                                                                                    1 GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
                                                               GQGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFS
                                                                                                                                         100.0%; S ilarity 100.0%; P Conservative 0;
                                                                                                                                         Score 1536; DB 11;
Pred. No. 7.4e-149;
0; Mismatches 0;
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                                                                                                                                                                              Length
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                                                                                                                                           Gaps
                        120
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APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PA:
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-09-02
PRIOR PILING DATE: 2000-08-12
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR SOFTWARE: FASESEQ for Windows Version 3.0
                                                                                        RESULT 3
US-09-918-715-232
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US-09-918-715-187
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Sequence 232, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 187
LENGTH: 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 295;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                      ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
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b. US20030017157A1
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Pred. No. 1.2e-148;
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APPLICANT: Barger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASS
TITLE OF INVENTION: THEXAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2RNM
CURRENT FILING DATE: 2002-11-21
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 564
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CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR PILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 232
LENGTH: 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 199, Application US/10301822 Publication No. US20030148410A1
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Best Local
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TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Millennium Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Pred. No. 1.2e-148;
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Tanng, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT APPLICATION UNMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FRSETSEQ for Windows Version 4.0
SEQ ID NO 1823
LENGTH: 564
TYPEB: PRT
ORGANISM: Homo sapiens
US-10-408-765A-1823
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US-10-408-765A-1823
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/ ORGANISM: Homo Sapiens
US-10-301-822-199
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Best Local S
Matches 295
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Similarity 100.0%; Pred. No. 1.2e-148;
95; Conservative 0; Mismatches 0;
                   ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 240
                                                                                                         ALTDGELHEDLFFYSERBANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQ 180
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ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT
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Sequence 232, Application US/10474794

Publication No. US20040213793A1

GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Vinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/382,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR APPLICATION NUMBER: 60/308,829
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; ORGANISM: Homo sapiens
US-10-474-794-187
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LENGTH: 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 295;
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Best Local
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PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FABRISEQ for Windows Version
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CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
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APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
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Pred. No. 1.2e-148;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-18
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US-10-474-794-232
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US-10-038-307-18
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SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 18
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/10038307

Publication No. US20030134786A1

GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Undith J. HEALEY
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICANTON NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
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Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 232
LENGTH: 564
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Best Local Similarity
Matches 294; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                   99.7%; Score 1532; DB 14
100.0%; Pred. No. 3e-148;
tive 0; Mismatches 0
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CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-02-66, 931
PRIOR FILING DATE: 2000-12-69
PRIOR FILING DATE: 2000-12-69
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 620
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US-09-833-245-620
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US-10-201-292-18
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Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
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Best Local (
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APPLICANT: Theresa L. O'KEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-293-293
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEO ID NOS: 36
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TYPE: PRT
ORGANISM: Homo s
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LENGTH: 4
TYPE: PRT
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No. US20030144193A1
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100.0%; Pred. No. 3e-148;
tive 0; Mismatches 0
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; OTHER INFORMATION: X
; NAME/KEY: SITE
; LOCATION: (368)
; OTHER INFORMATION: X
US-09-833-245-620
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US-09-796-753-12
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Publication No. US20030027998A1
GENERAL INFORMATION:
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   PRIOR
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TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7953-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: NAME/KEY: SITE LOCATION: (331)
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NAME/KEY: SITE
LOCATION: (320)
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NAME/KEY: SITE
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            OR APPLICATION NUMBER: 09/183,175
OR FILING DATE: 1998-10-30
OR APPLICATION NUMBER: 09/223,094
OR FILING DATE: 1998-12-30
OR APPLICATION NUMBER: 09/223,546
OR APPLICATION NUMBER: 09/223,546
OR APPLICATION NUMBER: 09/224,246
OR FILING DATE: 1998-12-30
OR APPLICATION NUMBER: 09/259,388
OR FILING DATE: 1999-02-26
OR APPLICATION NUMBER: 60/122,458
OR FILING DATE: 1999-03-01
OR APPLICATION NUMBER: 09/312,359
OR FILING DATE: 1999-05-14
OR APPLICATION NUMBER: 09/312,359
OR FILING DATE: 1999-06-18
OR APPLICATION NUMBER: 09/342,687
OR FILING DATE: 1999-06-19
OR APPLICATION NUMBER: 09/342,687
OR FILING DATE: 1999-06-9
OR APPLICATION NUMBER: 09/345,464
OR APPLICATION NUMBER: 09/345,464
OR APPLICATION NUMBER: 09/345,464
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Pred. No. 1.3e-147;
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; Sequence 2, Application US/10038307; Publication No. US20030134786A1; GENERAL INFORMATION:
; APPLICANT: James B. ROTTMAN
; APPLICANT: Theresa L. O'KEEFE; APPLICANT: Engin OZKAYNAK; APPLICANT: Judith J. HEALEY; TITLE OF INVENTION: Tango 197 and Ta; FILE REFERENCE: 7853-253-999
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US-10-038-307-2
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; NUMBER OF SEQ ID NOS:
; SEQ ID NO 12
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-12
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Best Local Similarity
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PRIOR FILING DATE: 2000-09-30
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and Tango 216 Compositions

and Methods

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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and
FILE REFERENCE: 7853-253-99
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FRETSEQ for Windows Version 4.0
SEQ ID NO 2
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US-10-201-292-2
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; ORGANISM: Homo sapiens
US-10-038-307-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-2
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CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
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Best Local Similarity
Matches 292; Conser
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Publication No. US20030144193A1
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Best Local
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ALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVT 240
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100.0%; Pr
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Pred. No. 2.5e-147;
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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Lodith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-24
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                                                                                        Sequence 24, Application US/10201292
Publication No. US20030144193A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-99
CURRENT APPLICANTION UNMEER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/10038307 Publication No. US20030134786A1 GENERAL INFORMATION:
                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 345
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Best Local Similarity
TYPE: PRT
ORGANISM: Homo
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sapiens
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Pred. No. 2.6e-147;
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PIR 79:*
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2: pir2:*
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Pred. No. is the number of results predicted becore greater than or equal to the score of the and is derived by analysis of the total score distribution

SUMMARIES

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transposase (04) B	probable chaperone	hypothetical prote	undulin 1 - human	integrin alpha-1 c	integrin alpha-E c	inter-alpha-inhibi	transcription regu	probable retroelem	integrin alpha-1 -	hypothetical prote	collagen alpha 3(V	dnaK protein NMB05	collagen alpha 3(V	hypothetical prote	hypothetical prote

ALIGNMENTS

	RESULT 1 REHULB 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	cell Burlace glycoprocein Cullo precursor (validated) - numan N;Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Mac eukocyte integrin alpha chain; neutrophil adherence receptor alpham chain
	C;Species: Homo sapiens (man) C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
	C;Accession: A31108; A28915; Ā41600; A30892; A32218; A46526; A26091; I52567 R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
	J. Biol. Chem. 263, 12403-12411, 1988 A:Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3. CDI
	A;Reference number: A31108; MUID:88315033; PMID:2457584 A;Accession: A31108
dicted by chance to have a	A; Molecule type: mRNA
re of the result being printed,	3 <cor></cor>

type 3, CD1

A;Cross-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A;Note: part of this sequence was confirmed by protein sequencing
R;Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
A;Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor McA;Reference number: A28915; MUID:88257215; PMID:2454931
A;Accession: A28915

A;Molecule type: mRNA
A;Residues: 1-499,501-965,'P',967-1153 <ARN'
A;Residues: 1-499,501-965,'P',967-1153 <ARN'
A;Residues: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594:
A;Note: the authors translated the codon TAC for residue 1129 as Thr
A;Note: part of this sequence, including the amino end of the mature protein, was confirm
R;Shelley, C.S.; Arnaout, M.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A;Title: The promoter of the CD11b gene directs myeloid-specific and developmentally regular regression: A41600; MUID:92073318; PMID:1683702

A; Molecule type: DNA A; Residues: 1-9 < SHE>

A;Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215
R;Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G.
Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988
A;Title: Molecular cloning of the alpha-subunit of human and guinea pig leukocyte adhesic A;Reference number: A94193; MUID:88190151; PMID:2833753

A; Accession: A30892

A;Molecule type: mRNA A;Residues: 917-1042 <AR2>

A;Cross-references: GB:M18044
R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: cDNA sequence for the alpham subunit of the human neutrophil adherence A;Reference number: A32218; MUID:89098893; PMID:2563162
A;Accession: A32218 receptor

A; Molecule type: mRNA A; Residues: 9-1153 <HIC>

A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home (;Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>
F;17-1108/Domain: extracellular #status predicted <EXT>
F;148-318/Domain: extracellular #status predicted <EXT>
F;1465-473/Region: calcium/magnesium binding #status predicted 
F;530-538/Region: calcium/magnesium binding #status predicted 
F;530-501/Region: calcium/magnesium binding #status predicted 
F;530-601/Region: calcium/magnesium binding #status predicted 
F;530-601/Region: calcium/magnesium binding #status predicted 
F;1109-1134/Domain: transmembrane #status predicted <TMM>
F;1109-1134/Domain: intracellular #status predicted <TMM>
F;1135-153/Domain: intracellular #status predicted <TMM>
F;1135-153/Domain: transmembrane #status predicted <TMM>
F;1109-134/Domain: transmembrane #status predicted 
                                     RESULT
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R;Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
A;Title: Characterization of the myeloid-specific CD11b promoter.
A;Reference number: IS2567; MUID:92144986; PMID:1346576
A;Accession: IS2567
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A;Note: the last three bases of intron 13, CAG, are included in some but not all matur A;Note: sequence extracted from NCBI backbone (NCBIP:121963)
R;Piarce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
Biophys. Acta 874, 368-371, 1986
A;Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across A;Reference number: A90664; MUID:87076671; PMID:3539202
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A;Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha-ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:12059:
A;Map position: 16p11.2-16p11
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A;Molecule type: DNA
A;Residues: 1-9 <RES>
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A;Residues: 1-499,501-1153 <FLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: not compared with conceptual translation
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leming, J.
        surface
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                                                                                                                                                                                                                                                                                      175
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glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTFKEFQNNPNPRSLVKPITQLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT 257
                                                                                                                                                                                                       VNN-FEALKTIQNQLREK----IFAIEGTQTGSSSSFEHEMSQEGFSAA
                                                                                                                                                                                                                                                                                  VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 223
                                                                                                                                                                                                                                                                                                                                                                     DGEKFGDPLGYEDVIPEADRE----GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                            DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR----IADS--KDHVFP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIAFLIDGSGSIIPHDFRRMKEFVST-----VMEQLKKSKTLFS-----LMQYSEEFRIH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLYFILDKSGSVL-HHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTED----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.5%; Score 145.5; DB
26.2%; Pred. No. 0.0016;
tive 45; Mismatches 8
        CD11c
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    precursor
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    C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-
C;Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811
                                                                                                                                                                                                       RESULT 3
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                                                                                                                        N; Alternate names: fibrochimerin
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                                                                                                                                                             collagen alpha 1(XII) chain precursor -
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A;Molecule type: DNA
A;Residues: 1-1163 <COR>
A;Residues: 1-1163 <COR>
A;Residues: 1-1163 <COR>
A;Cross-references: UNIPROT: P20702
A;Note: this revision to the sequence from reference A35543 includes the carboxyl
A;Note: this revision to the sequence from reference A35543 includes the carboxyl
A;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
J. Biol. Chem. 265, 2782-2788, 1990
A;Fitle: Genomic structure of an integrin alpha subunit, the leukocyte p150,95 mol
A;Reference number: A35543; MUID:90153906; PMID:2303426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 16p11.2-16p11.2

C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol C;Superfamily: cell surface glycoprotein; heterodimer; magnesium; tandem repeat; C;Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat; F;1-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence glycoprotein CD11c #status predicted <MAT>
F;20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F;20-1107/Domain: extracellular #status predicted <EXT>
F;149-319/Domain: von Willebrand factor type A repeat homology <VWA4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830 A;Note: part of this sequence was confirmed by protein sequencing C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: this sequence has been revised in reference A36584 R;Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Spi EMBO J. 6, 4023-4028, 1987 A;Title: cDNA cloning and complete primary structure of the A;Reference number: S00864; MUID:88166645; PMID:3327687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: leukocyte adhesion receptor p150 c;Species: Homo sapiens (man) C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 C;Accession: A36584; A35543; S00864 R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A. J. Biol. Chem. 265, 12750-12751, 1990 A;Reference number: A36584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1108-1133/Domain: transmembrane #status predicted <TMM>F;1134-1163/Domain: intracellular #status predicted <INT>F;61,89,392,697,735,899,939,1050/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: GDB:ITGAX; CD11C
A;Cross-references: GDB:119758; OMIM:151510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-755, 'L', 757-1163 < CO3 >
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A; Residues: 1-834 <CO2>
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                                                                                                                                         SLDYKD-VIPMADAAGIIRYAIGVGLAFQNRNSWKELND-----IASKPSQEHIFKVED-
                                                                                                                                                                                                                                                                                  NPLSLLASVHQLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE--
                                                               FOALOGIIHSILKKSCIEILAAEPSTICAGESFOVVVRGNGF
                                                                                                                                                                                                               LFFYSEREANRSRDLGAIVYCVGV------KDFNETQLARIAD--SKDHVFPVNDG
                                                                                                                                                                                                                                                                                                                                                     ---QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTAS-VIIALTDGELHED
FDALKDIQNQLKEK----İFAIEGTETTSSSSFELEMAQEGF
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                                                                                                                                                                                                                                                                                  -GFTYTATAIQNVVHRLFHASYGARRDATKILIVITDGKKEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 143.5; DB Pred. No. 0.0024; 3; Mismatches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9;
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chicken

09-Jul-2004

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A; Introns: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1 (CREYWORDS: alternative splicing; cell binding; coiled coil; connective ti F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-3124/Product: coilagen alpha I(XII) chain #status predicted <MAT>
F;24-114/Domain: IIIA #status predicted <IIIA |
F;24-114/Domain: IIIA #status predicted <IIIA |
F;24-115/Domain: ribronectin type III repeat homology <FN3A>
F;137-301/Domain: Fibronectin type III repeat homology <FN3B>
F;137-301/Domain: Fibronectin type III repeat homology <FN3B>
F;332-414/Domain: Fibronectin type III repeat homology <FN3B>
F;337-601/Domain: Von Willebrand factor type A repeat homology <VWA2>
F;332-1178/Domain: IIIC #status predicted <IIIC>
F;629-1178/Domain: &fbronectin type III repeat homology <VWA2>
F;630-711/Pypasin: &fbronectin type III repeat homology <VWA2>
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A;Residues: 2960-2976, F;,2978-3074,'AG' <GOR3>
A;Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1;
A;Note: this sequence has been revised in reference A34485
A;Koch, M.; Bernasconi, C.; Chiquet, M.
Bur. J. Biochem. 207, 847-856, 1992
A;Title: A major oligomeric fibroblast proteoglycan identified A;Reference number: $23814; MUID:92362621; PMID:1323460
A;Accession: $23814
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Biochim. Biophys. Acta 1171, 97-98, 1992
A;Title: The two splice variants of collagen XII share a
A;Reference number: $28811; MUID:93042014; PMID:1420368
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A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517
R;Dublet, B.; van der Rest, M.
J. Biol. Chem. 262, 17724-17727, 1987
A;Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsia A;Reference number: $22254; MUID:88087065; PMID:3121603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 2772-2792;2846-2873 <GOR2>
R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix A;Reference number: A28037; MUID:87317590; PMID:3476925
A;Accession: A28037.
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A;Residues: 1-3124 <YAM>
A;Residues: 1-3124 <YAM>
A;Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; GB:D00824; NID:g222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; PIDN:G222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; PIDN:G222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P1394; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROT:P13944; PIA;Cross-references: 
F;995-1076/Domain: fibronectin type III repeat homology <FN3G>
F;1086-1169/Domain: fibronectin type III repeat homology <FN3H>
F;1197-1361/Domain: von Willebrand factor type A repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X67327
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A; Residues: 1-24, 1189-1257, 'S', 1259-1263, 'E', 1265-1280 <TRU>
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A; Residues: 2831-2832,'T',2834,'R',2836-2843;3002-3014 <DUB:
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A;Title: Type XII collagen. A large multidomain molecule with partial homology to
A;Reference number: A34485; MUID:90062079; PMID:2584192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S22254
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J. Cell Biol. 115, 209-221, 1991
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1721-802/Domain: fibronectin type III repeat homology <FN3D>
1812-895/Domain: fibronectin type III repeat homology <FN3E>
1805-986/Domain: fibronectin type III repeat homology <FN3E>
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F;1384-1465/Domain: fibronectin type III repeat homology <FN3I>
F;1474-1557/Domain: fibronectin type III repeat homology <FN3I>
F;1465-1647/Domain: fibronectin type III repeat homology <FN3I>
F;1565-1637/Domain: fibronectin type III repeat homology <FN3I>
F;1655-1738/Domain: fibronectin type III repeat homology <FN3I>
F;1647-1928/Domain: fibronectin type III repeat homology <FN3I>
F;1847-1928/Domain: fibronectin type III repeat homology <FN3I>
F;1937-2019/Domain: fibronectin type III repeat homology <FN3I>
F;2028-2110/Domain: fibronectin type III repeat homology <FN3IP>
F;2119-2199/Domain: fibronectin type III repeat homology <FN3IP>
F;2119-2199/Domain: fibronectin type III repeat homology <FN3R>
F;2207-2294/Domain: fibronectin type III repeat homology <FN3R>
F;2325-2490/Domain: von Willebrand factor type A repeat homology <WAA>
F;2438-2440/Region: cell adhesion #status predicted <CCL2>
F;2438-2440/Region: cell adhesion #status predicted <CCL2>
F;251-2902/Domain: collagenous COL2 #status predicted <CCL2>
F;2903-2904/Region: cell attachment (R-G-D) motif
F;2904-3104/Region: cell attachment (R-G-D) motif
F;2904-3104/Domain: non-collagenous NC1 #status predicted <CCL1>
F;2946-3048/Domain: collagenous COL1 #status predicted <CCL1>
F;2969-3104/Domain: non-collagenous NC1 #status predicted <CCL1>
F;2969-3104/Domain: collagenous NC2 #status predicted <CCL1>
F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukocyte surface glycoprotein Mac-1 alpha chain precursor N;Alternate names: complement-3 receptor alpha chain C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence revision 30-Sep-1991 #text_ch C;Accession: S00551; I59078
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S00551
                                                                                                                                                                        A;Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983 A;Note: the authors translated the codon CAC for residue 569 as Gln R;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.B.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986 A;Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept A;Reference number: 159078; MUID:86287312; PMID:2942940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBO J. 7, 1371-1378, 1988
A;Title: Amino acid sequence of the murine Mac-1 alpha chain A;Reference number: S00551; MUID:88312584; PMID:3044779
A;Accession: S00551
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A; Residues: 1-1153 < PYT>
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A; Residues: 11-44 < RES>
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A;Cross-references: GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193
                                                                                                      A; Status: preliminary; translated
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Pred. No. 0.0098;
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A;Cross-references: UNIPROT:Q04588; GB:M99058; NID:g158890; PID:g158891
A;Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)
F;45-218/Domain: von Willebrand factor type A repeat homology <VWA2>
F;238-296/Domain: thrombospondin type 1 repeat homology <THR1>
F;309-371/Domain: thrombospondin type 1 repeat homology <THR2>
F;372-432/Domain: thrombospondin type 1 repeat homology <THR3>
F;433-493/Domain: thrombospondin type 1 repeat homology <THR4>
F;474-556/Domain: thrombospondin type 1 repeat homology <THR5>
F;460-610/Domain: thrombospondin type 1 repeat homology <THR6>
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Mol. Biochem. Parasitol. 57, 171-174, 1993
A;Title: Sequence of a major Eimeria maxima antigen homologous
A;Reference number: A48569; MUID:93149203; PMID:8426611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Eimeria maxima
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A48569
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A;Residues: 1-724 <PAS>
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                                                                                          SDSRAQNADLLAAAAKKLPYAAGSTYTHLGLAKA-EEILFSFQKGGRDNAPKMILVMTDG
                                                                                                                                                                                                                                  CYGGFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKL
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                                            ELHEDLFFYSERE-----ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP-
                                                                                                                                       TEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDG 125
                                                                                                                                                                                        CTRLLDVMLVVDESGSIGTSNYGKVRSFISNFAGTMPLSPDDVRVGLVTFGTSAVTRWDL 101
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24.2%; Pred. No. 0.0038;
tive 50; Mismatches 96; Indels 7
                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                                                                                                                                                      Score 139; DB 2
Pred. No. 0.003;
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A;McCcule type: protein

A;McCcule type: protein

A;Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
C;Reywords: alternative splicing; coiled coil; extracellular matrix; glycor

F;40-204/Domain: town Willebrand factor type A repeat homology <FW3A>
F;236-317/Domain: fibronectin type III repeat homology <FW3B>
F;236-409/Domain: fibronectin type III repeat homology <FW3B>
F;418-498/Domain: fibronectin type III repeat homology <FW3D>
F;625-707/Domain: fibronectin type III repeat homology <FW3D>
F;625-707/Domain: fibronectin type III repeat homology <FW3B>
F;716-798/Domain: fibronectin type III repeat homology <FW3B>
F;716-798/Domain: fibronectin type III repeat homology <FW3G>
F;924-1089/Domain: non-collagenous NC4 #status predicted <NC4>
F;1511-1553/Domain: non-collagenous NC4 #status predicted <NC2>
F;1511-1559/Domain: triple helical domain COLI #status predicted <COL1>
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A; Residues: 1-1747 <GBK>
A; Cross-references: UNIPROT: P32018
A; Cross-references: UNIPROT: P32018
A; Experimental source: embryo skin
A; Experimental source: embryo skin
b; Experimen
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A;Residues: 286-494, '0', '496-834, 'A',836-1119, 'KL',1122-1402,1409-1439 <TRU>
A;Residues: 286-894, '0', 496-834, 'A',836-1119, 'KL',1122-1402,1409-1439 <TRU>
R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, Eur. J. Biochem. 201, 333-338, 1991
Eur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens A;Reference number: S17035; MUID:92037585; PMID:1935930
A;Accession: S17035
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A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
A;Accession: S22916
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A;Reference number: $30085
A;Accession: $30085
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C;Date: 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974, S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, J. Biol. Chem. 268, 12177-12184, 1993
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A; Residues: 1472-1659 < GOR1>
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A; Residues: 1472-1660 < APT>
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A; Residues: 1-1747 <GER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: undulin
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                                                                                                 926 DLVFLVDGSWSIGDDNFNKIISFLYSTVGÅLDKIGPDGTQVAIIQFSDDPRTEFKLNAYK 985
                                                                                                                                                                                                                                                                                          63,
                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                         DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E
DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE
                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                 Score 137; DB 2
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                     Mismatches
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RESULT 8
C2MS
Classical-complement-pathway C3/C5 convertase (EC 3.4.21.43) C2 c
NJAlternate names: C3 convertase; C5 convertase; complement C2
NJAlternate names: C3 convertase; C5 convertase; complement C2
CjSpecies: Mus musculus (house mouse)
CjDate: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change
CjDate: 30-Sep-1993 #sequence revision 30-Sep-1993 #sequence 
submitted to GenBank, Janu A;Reference number: A38875 A;Accession: A38876
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A;Note: Bequence extracted from NCBI backbone (NCBIN:77752, NCBIP:77756)
F;48-218/Domain: von Willebrand factor type A repeat homology <VWAL>
F;238-296/Domain: thrombospondin type 1 repeat homology <THR2>
F;339-371/Domain: thrombospondin type 1 repeat homology <THR2>
F;309-371/Domain: thrombospondin type 1 repeat homology <THR2>
F;337-432/Domain: thrombospondin type 1 repeat homology <THR2>
F;339-393/Domain: thrombospondin type 1 repeat homology <THR4>
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A;Title: Sequence of the gene encoding an immunodominant microneme A;Reference number: A45638; MUID:92131064; PMID:1775171
A;Accession: A45638
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A;Residues: 1-712 <TOM>
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RESULT 9 S31212

collagen alpha 1(XIV) chain precursor, C;Species: Gallus gallus (chicken)

short torm

chicken

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A; Introns: 16/1
C; Complex: The J
C; Function:
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A;Pathway: complement b/C2; complement factor H repeat homology; trypsin homology; vc
C;Reywords: alternative splicing; complement classical pathway; duplication; glycoproteir
F;1-18/Domain: signal sequence #status predicted <SIG>
F;10-250/Product: complement C2b fragment #status predicted <C2B>
F;22-89/Domain: complement factor H repeat homology <FH2>
F;94-149/Domain: complement factor H repeat homology <FH2>
F;551-760/Product: complement factor H repeat homology <FH2>
F;251-760/Product: complement C2a fragment homology <FH3>
F;251-760/Product: complement C2a fragment homology <FFA>
F;251-49/Domain: von Willebrand factor type A repeat homology <VFA>
F;259-449/Domain: von Willebrand factor type A repeat homology <VFA>
F;478-747/Domain: trypsin homology #status atypical <TRY>
F;479-499.99.41-316,122-149,156-197,182-210,470-590,499-515,593-609,647-674,685-715/DistF;27,117,297,340,474,478,663/Binding site: carbohydrate (Asn) (covalent) #status predicted F;514,570,689/Active site: His, Asp, Ser #status predicted
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A;Title: Murine complement C2 and factor B genomic and cDNA cloning reveals different me A;Reference number: A36593; MUID:91035430; PMID:2229060
A;Accession: B36593
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A;Title: DNA polymorphism of MHC III genes in inbred and wild mouse strains.
A;Reference number: I54429; MUID:87192938; PMID:2883115
A;Accession: I54429
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A;Cross-references: UNI
R;Ishikawa, N.; Nonaka,
J. Biol. Chem. 265, 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 660-677, 'R', 679, 681-723, 'G', 725
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A; Residues: 1-760 < ISH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHLNLYLLLDASQSVTEKDFDIFKKSAELMVERIFSFEVNVTVAIITFASQPKTIMSILS
VGDPTSQHGKEFLVEDVII
                                                        MND----GLSFISSSVII
                                                                                                                GNMSANASDQERTPWQVTFKPKSKETCQGS--LISDQWVLTAAHCFHDIQMEDHHLWRVN
                                                                                                                                                                           GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS 272
                                                                                                                                                                                                                                      LNE--LGSKKDGERHAFILQDA-KALQQIFEHMLDVSKL
                                                                                                                                                                                                                                                                                              FNETQLARIADSKDHVFPVNDGFQALQGIHSILKKSCIEILAAEPSTICAGESFQVVVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERSQ-----DVTEVITSLDSASYKDHENATGANTYEVLIRVYSMMQTQMDRLGMETSAW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTE
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PIDN:AAA39562.1; PID:g199290
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into C2a,
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A;Residues: 1-1888 <TRU>
A;Residues: 1-1888 <TRU>
A;Cross-references: UNIFROT:P32018; EMBL:X70793; NID:g288872; PIDN:CAA50064.1;
A;Cross-references: UNIFROT:P32018; EMBL:X70793; NID:g288872; PIDN:CAA50064.1;
R;Maelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A:Reference number: S31211; MUID:93185668; PMID:8444186
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F;442-525/Domain: fibronectin type III repeat homology <FN3C>
F;534-614/Domain: fibronectin type III repeat homology <FN3C>
F;623-707/Domain: fibronectin type III repeat homology <FN3E>
F;623-707/Domain: fibronectin type III repeat homology <FN3E>
F;741-923/Domain: fibronectin type III repeat homology <FN3F>
F;832-1009/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3G>
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A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
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$collagen alpha 1(XIV) chain precursor, long form -
$collagen alpha 1(XIV) chain precursor, long f
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                                       A;Reference number: S31211;
A;Accession: S31211
A;Status: preliminary
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A; Accession: S78476
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A; Residues: 1-1857 <WAE>
A; Molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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25.0%; Pred. No. 0.055;
tive 44; Mismatches 116; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               January 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:CAA50063.1; PID:g288875 to the EMBL Data Library, January
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GFKMMEMFGLVEKEFSAIDGVSMEPGTF 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -FDAFTKIE
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                                                                                                                                                                                                                                                                                                                                      PID: 92888
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A;Gene: Coil4Al

C;Keyworde: alternative splicing; coiled coil; extracellular matrix; glycoprotein;
F;1-28/Domain: signal sequence #status predicted <SIG>
F;1-28/Pomain: signal sequence #status predicted <SIG>
F;2-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;35-320/Domain: fibronectin type III repeat homology <FN3B>
F;35-43/Domain: fibronectin type III repeat homology <FN3D>
F;442-525/Domain: fibronectin type III repeat homology <FN3D>
F;623-707/Domain: fibronectin type III repeat homology <FN3F>
F;741-823/Domain: fibronectin type III repeat homology <FN3F>
F;332-914/Domain: fibronectin type III repeat homology <FN3F>
F;832-914/Domain: fibronectin type III repeat homology <FN3F>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;932-1009/Domain: fibronectin type III repeat homology <FN3G>
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S42373
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A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                            F;754-793/Domain: fibronectin type 11 1
F;1201-1244/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-3051 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data A; Reference number: S42368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Caenorhabditis elegans; Date: 07-Oct-1994 #sequence_revision
                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
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Best Local
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ELFEIGRSKTRVGLIQYSDQIRHEFDLDQYGDRDSLLKGISETQ-YLTGLTRTGAAIQHM
                                                                                                                                                                                              CYGGF---
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                                                           HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH-
                                                                                                                            CYGGFVDVSSNANLPPGRVCTVQTTCPKQKTDLVFLIDGSGSIGSYVPKNEVLRFVREFV 542
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                                                                                                                                                                                                                                                      Conservative
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25.0%; Pred. No. 0.
                                                                                                                                                                                                                                                   8.3%; Score 128; DB 2; Length 3051; 27.1%; Pred. No. 0.16; tive 31; Mismatches 75; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;
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                                                                                                                                                                                              DLYFILDKSGSVLHH--WNEIYYFVEQLA 44
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         601
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Cartilage matrix protein precursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004 C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004 C;Date: 12-Jul-1999; B37979 C;Accession: A37979; B37979 S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh J. Biol. Chem. 265, 19624-19631, 1990 J. Biol. Chem. 265, 19624-19631, 1990 A;Title: Structure and chromosomal location of the human gene encoding cartilage matrix A;Reference number: A37979; MUID:91060568; PMID:2246248
A;Molecule type: mRNA
A;Residues: 157-290,'L',292-496 <JE2>
A;Cross-references: GB:M55683; GB:J05666; GB:J05667; NID:g180651; PIDN:AAA63904.1;
C;Genetics:
                                                                                                                                     A;Residues: 1-496 <JEN>
A;Cross-references: UNIPROT:P21941;
                                                                                                                                                                                                                   A; Reference number: A37979;
A; Accession: A37979
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F;155-236/Domain: fibronectin type III repeat homology <3FR>
F:631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-20
                                                                                                                                                                                       A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A37979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-929 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
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Y.; Yang, b...
168, 503-513,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSVEDTYLLCPAPILKEVGMKAALQVSMN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TENVCNSVKGPGGLNPPSNLVTSEPTPRSPRVTWVPPSQSVER---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKKSCIEILAA----EPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IVAPSKRYA----DEGIELYAVGIKNADENELKETASDPDELYMYNVADFSLLTNIVNDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQEGF-----SERRGARPQQSDIARVAIILTDGRSQDNV----TGPADSARKLSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGY----RTASVIIALTDGELHED 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFAIGVTDHVLASELESIAGSPNRWFYV-DKFKDLDTRLRSMIQK-----AACPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E.V.; Klatt, K.P.; Tassava, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.7%; Score 118; DB 2; Length 929
21.2%; Pred. No. 0.21;
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                                                                                                                                     GB:J05667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          887
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A;Molecule type: mRNA
A;Residues: 467-546;550-595;752-764 <WOO>
A;Cross-references: GB:J00185; GB:J00186
A;Note: the authors translated the codon TAC at 519 as Thr; tl
A;Nole; J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.E.
Clem. 259, 3407-3412, 1984
A;Title: Complete primary structure for the zymogen of human a, Reference number: A20751; MUID:84161997; PMID:6546754
A;Accession: A00934
A;Note: glycosylation sites were R;Christie, D.L.; Gagnon, J. Biochem. J. 209, 61-70, 1983
A;Title: Amino acid sequence of t
                                                                                                                                                                   A; Molecule type: protein; mRNA
A; Residues: 26-764 < MOL>
A; Cross-references: GB: K01566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P00751; EMBL:X72875; NID:g297568; PIDN:CAA51389.1; R;Woods, D.E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, H.R. Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982
A;Title: Isolation of cDNA clones for the human complement protein factor B, a A;Reference number: A44622; MUID:83039428; PMID:6957884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S34075
A; Accession: S34075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 19-Feb-1984 #sequence revision 05-Aug-1994 #text change 09-Ut
C;Date: 19-Feb-1984 #sequence revision 05-Aug-1994 #text change 09-Ut
C;Accession: S34075; A44622; A00934; A19188; A19947; B19947; B25971;
R;Mejla, J.B.; Jahn, I.; de la Salle, H.; Hauptmann, G.
submitted to the EMBL Data Library, March 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement factor B precursor [validated] - human
N;Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; heat-]
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragment
                                                                                                              A;Note: nucleic acid translation differs A;Note: 736-Ser was also found
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A; Residues: 1-764 < MEJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;23-496/Product: cartilage matrix protein #status predicted <MAT>
F;39-206/Domain: von Willebrand factor type A repeat homology <VWA1>
F;227-262/Domain: EGF homology <EGF>
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A;Map position: 1p35-1p35
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A44622
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26.0%; Pred. No. 0.2
                                                                                      determined
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                                                                                                                                              328-1
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Amino acid sequence of the

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Sequence

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A;Molecule type: mRNA
A;Residues: 339-509 <CAl>
A;Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
A;Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
R;Wu, L.; Morley, B.J.; Campbell, R.D.
Cell 48, 331-342, 1987
Cell 48, 331-342, 1987
A;Title: Cell-specific expression of the human complement protein factor B gene: evidend A;Reference number: A25971; MUID:87102880; PMID:3643061
A;Accession: B25971
                                                                                                                  A;Map position: 6p21.3-6p21.3
A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; A;Note: the list of introns may be incomplete
A;Note: gene is located in the major histocompatibility complex, class III region
C;Complex: complement factor B initially forms an inactive complex with complement factor C3b forming active C3/C5 convertase; Ba is released
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residuse: 16-225,'F',227-259 <MOR>
R;Schwaeble, W.; Luttig, B.; Sokolowe
Immunobiology 188, 221-232, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 270-329 <NIE>
A;Residues: 270-329 <NIE>
A;Residues: 270-329 <NIE>
A;Rote: binding site for carbohydrate to lysine under artificial conditions
A;Morley, B.J.; Campbell, R.D.
EMBO J. 3, 153-157, 1984
A;Title: Internal homologies of the Ba fragment from human complement component
A;Reference number: A44628; MUID:84158524; PMID:6323161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Niemann, M.A.; Bhown, A.S.; Miller, E.J.
Biochem. J. 274, 473-480, 1991
A;Title: The principal site of glycation of human complement A;Reference number: S14339; MUID:91174758; PMID:2006911
A;Accession: S14339
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Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983
A;Title: Molecular cloning and characterization of the gene coding for human complement A;Reference number: A19947; MUID:83273641; PMID:6308626
A;Accession: A19947
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;ReBidueB: 1-31, 'Q',33-764 <RE2>
A;Croos-references: GB:L15702; NID:g291921; PIDN:AAA16820.1;
C;Comment: 292-Cy8 has a free sulfhydryl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Human complement factor B: cDNA cloning, nucleotide A;Reference number: I57824; MUID:94067177; PMID:8247029 A;Accession: I57824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Human complement factor B: functional properties of a recombinant zymogen of th
A;Reference number: I54409; MUID:94041399; PMID:8225386
A;Accession: I54409
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A;Residues: 1-99 <WUL>
A;Cross-references: GB:M15082; NID:g187699; PIDN:AAA59625.1;
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A;Residues: 1-764 <RES>
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                                                                                                                                                                                                                                                                                                                                                                   ;Gene: GDB:BF
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ol. Immunol. 30, 1587-1592, 1993
                                                                 Description: Bb
                                                                                                                                                                                                                                                                                                                                    ;Cross-references: GDB:119726; OMIM:138470
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complement
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                                                                     convertase cleaves complement C3 alpha
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C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; vc(;Keywords: acute phase; complement alternate pathway; duplication; glycoprotein; hydrolafication; glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycoprotein; complement factor H repeat homology cFH1>
F;103-159/Domain: complement factor H repeat homology cFH2>
F;165-218/Domain: complement factor H repeat homology cFH3>
F;165-218/Domain: complement factor H repeat homology cFH3>
F;165-218/Domain: von Willebrand factor type A repeat homology cVFA>
F;482-752/Domain: trypsin homology #status atypical cTRY>
F;307-76,62-98,103-145,131-158,165-205,191-218,478-596,511-527,599-615,656-682,695-725/Diafication; gite: carbohydrate (Asn) (covalent) #status experimental
F;259-260/Cleavage site: Arg-Lys (complement factor D) #status experimental
F;526,576,699/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text chang
C;Accession: A54849; PH0844; S16316; I56328; A30296; I84686
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
Biol. Chem. 269, 20256-20262, 1994
A;Tible: Cloning of human type VII Collagen. Complete primary
A;Reference number: A54849; MUID:94327588; PMID:8051117
A;Accession: A54849
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A54849
A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Baue: Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
                                                                                              A;Molecule type: mRNA, A;Ao.475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', A;Residues: 'EFR',340-475, 'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', A;Croos-references: DDBJ:D11152; DDBJ:D13694; NID:g453698, PIDN:BAA02853.1, A;Experimental source: keratinocyte
A;Experimental source: keratinocyte
                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-2944 <CHR
A;Residues: 1-2944 <CHR
A;Cross-references: UNIPROT:Q02388; GB:L02870; NID:g987124; PIDN:AAA75438.1;
A;Cross-references: UNIPROT:Q02388; GB:L02870; NID:g987124; PIDN:AAA75438.1;
A;Teta-references: UNIPROT:Q02388; GB:L02870; NID:g987124; PIDN:AAA75438.1;
B;Cochen. Biophys. Res. Commun. 183, 958-953, 1992
A;Title: Molecular cloning and characterization of type VII collagen cDNA.
A;Reference number: PH0844; MUID:92231902; PMID:1567409
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Pred. No. 0.3
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                                     K.C.; Bauer,
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                                                                                                                                   ,524-528,'C',
PID:g453699
                                                                                                                                                                                                                                                                                                                                                                                                PID:g987125
                                        E.A.;
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P/954-1045/Domain: fibronectin type III repeat homology <PN9>
P/1052-1219/Domain: von Willebrand factor type A repeat homology <VWA2>
P/1170-1172/Region: cell attachment (R-G-D) motif
P/1189-1253/Region: cysteine/proline-rich
F/1254-2783/Region: interrupted helical
P/1334-1336/Region: cell attachment (R-G-D) motif
F/2008-2010/Region: cell attachment (R-G-D) motif
P/2553-2555/Region: cell attachment (R-G-D) motif
P/2553-2555/Region: cell attachment (R-G-D) motif
P/2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
P/2876-2924/Domain: animal Kunitz-type proteinse inhibitor homology <BPI
P/2876-2924/Domain: animal Kunitz-type proteinse inhibitor homology <BPI
P/2876-2924/Domain: animal Kunitz-type proteinse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P;17-1253/Domain: amino-terminal nonhelical #status predicted F;36-201/Domain: von Willebrand factor type A repeat homology F;231-319/Domain: fibronectin type III repeat homology <FN1>F;327-413/Domain: fibronectin type III repeat homology <FN2>F;414-502/Domain: fibronectin type III repeat homology <FN3>F;508-593/Domain: fibronectin type III repeat homology <FN4>F;508-693/Domain: fibronectin type III repeat homology <FN5>F;508-693/Domain: fibronectin type III repeat homology <FN5>F;776-862/Domain: fibronectin type III repeat homology <FN7>F;776-862/Domain: fibronectin type III repeat homology <FN7>F;986-952/Domain: fibronectin type III repeat homology <FN8>F;986-952/Domain: fibronectin type III repeat homology <FN8>F;9864-952/Domain: fibronectin type III repeat homology <FN8>F;9864-952/Domain: fibronectin type III repeat homology <FN8>F;9864-952/Domain: fibronectin type III repeat homology <FN8>FN8
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A;Residues: 2395-2871, 'S',2873-2944 <RE2>
A;Residues: 2395-2871, 'S',2873-2944 <RE2>
A;Cross-references: GB:L06862; NID:g388713; PIDN:AAA89196.1; PID:g388714
A;Christiano, A.M.; Ryymaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermoly9is bulloss: identification of a Gly --> Ser substance number: A55255; MUID:94224777; PMID:8170945
A;Contents: annotation
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit (ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxyly F;1-16/Domain: signal sequence #status predicted <SIG> F;17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 3p21.3-3p21.3
A;Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
A;Note: there are 118 introns
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A;Residues: 'EFR',372-517,'DV',520-540,'W',542-1255 <RES>
A;Residues: 'EFR',372-517,'DV',520-540,'W',542-1255 <RES>
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A;Cross-references: GB:S51236; NID:g262308; PIDN:AAB24637.1; PID:g26230
R;Seltzer, J.L.; Bisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.P.
J. Biol. Chem. 264, 3822-3826, 1989
A;Title: Cleavage of type VII collagen by interstitial collagenase and A;Reference number: A30296; MUID:89139437; PMID:2537292
A;Accession: A30296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hum. Mol. Genet. 2, 273-278, 1993
A;Title: The carboxyl-terminal half of type VII collagen, A;Reference number: I48103; MUID:93271985; PMID:8499916
A;Accession: I84686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright, J. Invest. Dermatol. 99, 691-696, 1992
A;Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion pro A;Raference number: 156328; MUID:93107742; PMID:1469284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Gene: GDB:COL7A1; EBR1; EBD1; EB; ;Cross-references: GDB:128750; OMIM:120120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: protein, Residues: 'A', 1240-1246,'G', 1248-1250,'XE', 1253-1255,'Q', 1257,'E', 2032,'C', 2034-2041, Note: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description: structural component of extracellular polymer; Reywords: coiled coil; extracellular matrix; glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complex: type VII collagen is probably a homotrimer
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Cross-references: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
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Glanville, R.W.; Burgeson,
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carbohydrate (Asn)

(covalent) #status

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LVSRRVCTTAGGVPVTRPPDDSTSAPRDLVLSEPSS
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1058	1172	1257	1299.5	1413	1499	1499	1499.5	1499.5	1501	1501	1504	1504	1509	1509	1509	1509	1514	1514	1514
69.3	76.8	82.4	85.2	92.6	98.2	98.2	98.3	98.3	98.4	98.4	98.6	98.6	98.9	98.9	98.9	98.9	99.2	99.2	99.2
460	479	297	504	529	540	540	342	342	328	328	549	384	562	562	562	562	564	564	549
7	7	4	7	7	7	7	7	7	7	7	7	7	σ	σ	ഗ	v	7	7	7
ADI00560	ADI00564	AAM38976	ADI00566	ADI00568	ADM64588	ADI00544	ADM64580	ADI00554	ADM64584	ADI00558	ADI00542	ADM64586	ABU54438	ABU54492	ABB90785	ABB90731	ADM64578	ADI00552	ADM64592
Human	Adi00564 Human TAN	Aam38976 Human pol	Adi00566 Human TAN	Adi00568 Human TAN	Adm64588 TANGO197	Adi00544 Human TAN	Adm64580 Human TAN	Adi00554 Human TAN	Adm64584 Human TAN	Adi00558 Human TAN	Adi00542 Human TAN	Adm64586 TANGO197	Abu54438 Mouse tum	Abu54492 Mouse tum	Abb90785 Mouse Tum	Mouse	Adm64578 Human TAN	Adi00552 Human TAN	Adm64592 TANGO197

ALIGNMENTS

RESULT 1 ABP54903 ID ABP5 XX ABP5 XX O8-J XX Huma XX Huma XX Anth XX Homc XX Homc FT Prot FT Regi Region Region Region Region Region Region 08-JAN-2003 ABP54903; WO200246228-A2 Domain Domain Protein Homo sapiens. Anthrax; toxin; ABP54903 standard; protein; 368 Domain Peptide Human anthrax toxin receptor (first entry) receptor; human; antibacterial. /note= /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 50, 52, 54 and 118" 320. .343 /note= "PA-binding fragment, begins at any amino acid in the range 27-43 and ends at any amino acid in the range 221-321, region specifically described in Claim 3" /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 50, 52, 54 and 150" motif with /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 50, 54, 118 and 150" /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 52, 54, 118 and 150" 28. .320 /note= "extracellular domain" 28. .368 Location/Qualifiers note= "forms metal ion-dependent amotif with amino acid residues 50, note= "von Willebrand factor A domain" 'label= Mature_protein /label= Signal_peptide "cytoplasmic domain" "putative transmembrane ₿ domain" adhesion), 52, 118 site (MIDAS) and 150"

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RESULT 2
AAE01439
ID AAE0
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AC AAE0
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DT 17-J
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DE Huma
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Best Local :
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   Human;
                                                                                                AAE01439;
                                                                                                                              AAE01439 standard; protein; 403 AA
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                                 Human gene 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated polypeptide useful for identifying agent that prevents or reduces effect of anthrax toxin on host cell, for treating human or non-
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                                                                                                                                                                                                                                                                                                                                                                                                                                            RGTTLMKLTEDREQIRQGLEBLQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA 120
                                                                                                                                                                                                                 NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG 320
                                                                                                                                                                                                                                     NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
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                                                                                                                                                                                                                                                                                                   LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL
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                                                                                                                                                                                                                                                                               LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL
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                              encoded secreted protein HWLFR02,
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                                                                (first entry)
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Pred. No. 1.5e-155;
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   disorder; cancer; tumour;
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                                   SEQ ID NO:94.
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The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.

CC Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 28 genes, compared to the new genes. Specific uses are described for each of the 28 genes, concert, tumours, foetal and developmental abnormalities, can disorders, cancer, tumours, foetal and developmental abnormalities, concert, tumours, foetal and developmental abnormalities, consisted disorders, diseases of the immune system, AIDS, autoimmune constitute disorders (e.g., Alaheimer's disease, Parkinson's disease), consistive disorders (e.g., Alaheimer's disease, Parkinson's disease), consistive disorders, schizophrenia, asthma, skin disorders (e.g., pregnancy-related disorders, and therosclerosis, cardiovascular disorders, cangiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell correlates, and in chemotaxis, and can be used as a food additive or prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to reservative to moder or supporting and can be used as a food additive or an analysis of the for a creary tissue of the for a supporting can also be used to an analysis or binding the supporting cell culture of primary tissues.
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                                                                                 preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid molecules encoding 28 human secreted proteins diagnosing, preventing, treating or ameliorating medical conditused as food additives or preservatives.
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                                                    or enzyme linked
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Sequence AA,

Query Match

100.0%; Score 1526; BB 4 Length 403

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ARESULT 3
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AD ABG6
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Matches
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25-APR-2000;
21-DEC-2000;
                     The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shalf-life of protein X, and may increase its biological in vitro/in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; cytostatic; anti-HIV; antidiabetic; haemostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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No. 1.8e-155;
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albumin fusion proteins,

useful for diagnosing,

treating,

preventing

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or ameliorating diseases or disorders e.g. cancer, anemia, arthritis asthma, inflammatory bowel disease or Alzheimer's disease.
SEQ ID NO 621; 279pp; English.
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CC disorder in a pattent comprising the step of administering the albumin CC (tusion protein; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; CC a method of extending the shelf life of Therapeutic protein: X, or its fragment or variant; CC a method of extending the shelf life of Therapeutic protein: X, or its comprising a polymucleotide comprising the nucleic acid molecule comprising a polymucleotide comprising the nucleic acid molecule of the albumin fusion protein. The comprising the nucleic acid molecule of the albumin fusion protein. The call comprising the nucleic acid molecule of the albumin fusion protein. The call comprisities: cytostatic, antianaemic, antiarthritic, antiasthmatic, antiatities: cytostatic, antianaemic, antiapout, antiapout, antiatic, antiacterial, costeopathic, dermatological, antigout, immunomodulator, antiarrhythmic, cardiant, nootropic, antilpaemic, nephrotropic, uropathic, anabolic, hypertensive, and vulnerary. The albumin fusion protein nucleic acid may be used in gene therapy to treat disorders. The albumin fusion protein acid may compressed in gene therapy to treat disorders. The albumin fusion protein is useful for diagnosing, treating, preventing or ameliorating diseases or compressive, and colon, bone, breast, liver or lung cancer), completed chaeses (e.g. anaemia, Hodgkin's disease, acute lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS, controlled con Sachs disease), excretory diseases (e.g. urinary incontinence, urinary tract infections or renal disorders), neural or sensory disease (e.g. Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis, cerebellar ataxia, attention deficit disorder, autism or obsessive compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or occupational lung disease), endocrine diseases (e.g. diabetes, Addison's disease or glomerulonephritis), digestive diseases (e.g. portal pypertension, irritable bowel disease, gastric atrophy or pancreatitis) or connective tissue or epithelial diseases (e.g. Crohn's disease, sclaroderma, wound healing or epithelial diseases (e.g. Crohn's disease, sclaroderma, wound healing or epithelial diseases bullosa). This sequence represents a therapeutic protein X relating to the albumin fusion protein of the invention. The sequence listing data for this specification was dowloaded from the USPTO website. or cachexia), cardiovascular disease (e.g. rhabdomyomas, heart disease, arrhythmia, cardiac arrest, heat valve disease, hypernatraemia or hyponatraemia), mixed foetal diseases (e.g. foetal alcohol syndrome, pown's syndrome, Patau syndrome, Turner's syndrome, Apert syndrome or Tay Sachs disease), excretory diseases (e.g. urinary incontinence, urinary Paget's disease, ther relates to: a composition comprising the albumin fusion protein a pharmaceutical carrier; a kit comprising the composition of the umin fusion protein formula; a method of treating a disease or systemic lupus erythematosus, to a novel albumin fusion protein. gout, muscular dystrophy The invention

Sequence 403

Matches Query Match Best Local !

293;

Conservative

Local

Similarity

Score 1526; DB 8; Pred. No. 1.8e-155; ; Mismatches 0;

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                                                                                                                                      RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA 120
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                                                                                                                                                                                                                  Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 45;
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HEALEY J J.
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                                                                                     The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a fusion protein comprising mouse TANGO197 and immunoglobulin (19) that can be used to treat exposure to or prevent a symptom of
                                                                                                                                                                                                                                                                          New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                     Sequence
                                                                                                                                                                                                                                        Claim 44; SEQ ID NO 18; 64pp; English
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                                                                                                                                                                                                                                                                                                                                                                           Rottman
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(HEAL/)
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sequence; anthrax; Bacillus anthracis; cutaneous
hrax; mouse; TANGO197; immunoglobulin; Ig; fusion
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11-AUG-2000;
11-APR-2001;
The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cyrostatic, immunostimulant and antianglogenic activity. They are useful for inhibiting tumour growth, neoanglogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psortiasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
                                                                                                                                                                                                                                                                                                                                                                                                     An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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Best Local :
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                                                                                       An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neonngiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endothelial markers (NEM) (PEM) ABL91903-ABL91995
 The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain tumour endothelial marker (TEM) protein selected from ABB90732, ABB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Tumour
                                                            Disclosure; Page 136-137; 331pp; English
                                                                                                                                                       WPI; 2002-291856/33.
                                                                                                                                                                                  St Croix B,
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11-AUG-2000;
                                                                                                                                                                                                                                                                                                       01-AUG-2001; 2001WO-US024031.
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                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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ilarity 100.0%;
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2000US-0224360P.
2001US-0282850P.
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                                                                                                                                                                                   Kinzler
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ABB90732, ABB90740,
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Best Local Similarity 100
Matches 293; Conservative
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                                03-OCT-2001; 2001WO-US030941.
                                                                                                                                                                                  Domain
                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                Anthrax; toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                Human anthrax toxin receptor
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                                                                  13-JUN-2002
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                                                                                                  WO200246228-A2
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Pred. No. 2.9e-155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the protein sequence of a human surface-bound CC anthrax toxin receptor (ATR), previously designated TEM6, and identified CC following a database screening using a newly isolated human surface-bound CC ATR (see ABP54903). The present sequence differs from the newly isolated CC human ATR only in the cytoplasmic domain (221 rather than 25 amino acids CC long), suggesting differential splicing of a primary mRNA transcript. CC Anthrax toxin protective antigen (PA) binds to these ATRs at a von CC willebrand factor A domain located in the extracellular domain of ATR. CC The invention provides ATR polypeptides and polymucleotides, vectors, CC methods for identifying molecules that bind the ATR and which reduce the toxicity of anthrax toxin. A claimed method for treating anthrax in a CC toxicity of anthrax toxin. A claimed method for treating anthrax in a CC toxicity of anthrax toxin a level effective to reduce the severity of between PA and ATR at a level effective to reduce the severity of CC anthrax. Suitable agents include the present polypeptide or a PA-binding CC affusion protein, a monoclonal or polyclonal antibody, a polysaccharide, a lipid or a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
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Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; pormal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis;
                                                                        Human tumour endothelial marker TEM 19.
                                                                                                              12-MAR-2003
                                                                                                                                                                                   ABU54457
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Pred. No. 2.9e-155;
Mismatches 0;
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treating human or non-
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
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06-FEB-2002;
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DB; ABX72029.
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                                                                                                                                                   LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQA
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                     NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
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                                                                 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL
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NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
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2002US-0354262P
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Pred. No. 2.9e-155;
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06-FEB-2002; 2002US-0354262P
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NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
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Leber's hereditary ontic names.
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17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1823; 180pp; English.
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CC for therapeutic intervention in treating a disease associated with a described mitochondrial function. Specifically, it refers to a method for contentifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The coresent invention describes a method for identifying such proteins that can be used in the treatment of various disease associated with altered continuous mitochondrial function including diabetes mellitus, huntington's disease, costeoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy cragged red fibre syndrome (MERRF) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticoronulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart composition of the invention. invention relates to novel mitochondrial targets that can be used

Sequence AA,

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Query Match
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 l Similarity
293; Conserv
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         100.0%;
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Score 1526; DB 7;
Pred. No. 2.9e-155;
Mismatches 0;
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                     564;
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| OGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST

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The present invention describes a method for detecting a pancreatic concer-associated transcript in a biological sample. The method comprises contacting the biological sample with a polynucleotide that selectively hybridies to a sequence at least 80% identical to a sequence as shown in any one of Tables 3 to 25 in the specification or having the GenBank CA Accession Number AP279145. Also described: (1) diagnosing pancreatic cancer in a human or animal subject being tested, determining the CC determining the subject having a pancreatic cancer will survive, or CC determining the suitability of a subject having a pancreatic cancer for CC surgical resection therapy, (2) detecting a pancreatic cancer-associated conversatic cancer will survive; and the polypeptide in a biological sample; (3) determining the likelihood that a subject having a pancreatic cancer. A pancreatic cancer-associated transcript has cytostatic activity, and can be used in Gene and protein therapy. A pancreatic cancer-associated transcript thas cytostatic activity, and can be used in gene and protein therapy. A pancreatic cancer-associated transcript concer-associated transcript cancer associated transcript cancer associ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting pancreatic cancer-associated transcript in a biological sample, useful for diagnosing or treating the disease, comprises contacting the sample with a polynucleotide that selectively hybridizes to a specific
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DB, ADR48215.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation; allergy; neurological disorder; Alzheimer's disease; inflammation; allergy; neurological disorder; schizophrenia; asthma; kkin disorder; peoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide or an antibody that binds to the isolated polypeptide can be used for diagnosing or prognosing pancreatic cancer or for preparing a medicament for the treatment of pancreatic cancer. The prognostic or diagnostic methods are useful for the early detection of pancreatic cancer or its metastases, and for monitoring the progress of disease such as during remission or following surgery or chemcherapy. The present sequence represents human tumour endothelial marker 8 precursor (TEM8), which is used in the exemplification of the present invention.
                                Misc-difference
                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene 4 encoded secreted protein HWLFR02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE01469 standard; protein;
                                                                                                                                                                                                                                                                                                          Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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Pred. No. 2.9e-155;
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"Encoded by

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CC protein genes, and AAE01436-AAE01513 represent the proteins they encode. CC AAE01514-AAE01544 represent human secreted protein fragments or variants. CC The genes and their secreted protein are useful for preventing, treating CC or ameliorating medical conditions, e.g., by protein or gene therapy. CC pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the 28 genes, and in a sample or by determining the presence of mutations in CC based on the tissues in which they are most highly expressed, and include CC developing products for the diagnosis or treatment of proliferative CC disorders, cancer, tumours, foetal and developmental abnormalities, autoimmune CC diseases (e.g., rheumatoid arthritis), inflammation, allergies, autoimmune CC diseases (e.g., rheumatoid arthritis), inflammation, allergies, cc cognitive disorders, kidney disorders, gastrointestinal disorders, cognitive disorders, kidney disorders, gastrointestinal disorders, cc angiogenic disorders, kidney disorders, gastrointestinal disorders, cc proteins can also be used to aid wound healing and epithelial cell cc proteins can also be used to oaid wound healing and epithelial cell cc proteins can also be used to oaid wound healing and epithelial cell cc protein of the invention can be used in alleviating symptoms associated correct of protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., cradioimmunoassays or enzyme linked immunosorbent assay (ELISA). The invention can be used in alleviating from invention of the invention of a human secreted in the invention of the invention.
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-308778/32
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30-JUN-2000; 2000US-0215133P.
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Best Local Sir Matches 291; Query Match Best Local

Similarity

99.7%;

Score 1515; DB 5; Pred. No. 2.7e-154;

Length 403;

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Gaps

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Mismatches

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                                                      The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and disgnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fusion protein albumin fused to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-APR-2000; 2000US-0229358P
25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
   Sequence
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Search completed: June 13, 2005, 19:56:50 Job time : 112.48 secs	NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSD 319	241 NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSD 292	B LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL 267		1 TDGELHEDLFFYSEREANRSRDLGAIXYCVGVKDFNETQLARIADSKDHVFPVNDGFQA 207	121 LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQA 180	B RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA 147	RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA 120	B QGGRREDGGPACYGGPDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST 87	QGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST 60

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodats/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodats/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodats/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodats/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodats/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodats/1/iaa/backfIles1.pep:*
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-08-462-652-46
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US-08-605-672-46
US-08-943-363-46
US-09-193-043-46
US-09-193-043-46
US-09-193-043-46
US-09-193-043-46
US-08-485-618-53
US-08-485-2939-53
US-08-943-363-53
US-08-948-3078-53
US-09-193-043-53
US-09-193-043-53
US-09-193-043-53
US-09-193-043-53
US-08-485-618-37
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US-08-485-618-37
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ALIGNMENTS

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US-08-286-889-46
                                                                                                                               ; MOLECULE TYPE: protein US-08-286-889-46
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GENERAL INFORMATION:
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                                                         Matches
                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,889

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: P38,659

REFERENCE/DOCKET NUMBER: 27866/32168

TELEPHONE: 312-474-6300
                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human 2 Integrin Alpha
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                           TELBFAX: 31.
TELBFAX: 25-3856
                                                                                                                                                                   TYPE: amino acid TOPOLOGY: linear
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                                                         Conservative
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28.2%;
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                                                       42; Mismatches
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Pred. No. 6e-09;
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                                                                                                                                                                                                                           TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4-
SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
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APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US
FILING DATE: 5-AUG-1994
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,618
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CTTY: Chicago
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                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                    NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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No. 5728533
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  PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                    PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 67
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                                                                              Conservative
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                                                                          10.9%; Score 166; DB 1; Length 1155; 28.2%; Pred. No. 6e-09; tive 42; Mismatches 96; Indels 3
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Best Local Similarity
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FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
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CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOTER: COMPUTER: PM PC COMPOTER: PC-DOS/MG-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
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CITY: Chicago
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TLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
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CLASSIFICATION: 435
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  TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                      FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKBLFHSKNGARKSAKKILIVI 258
                                                                           LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 121
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28.2%; Pred. No. 6e-09;
ative 42; Mismatches
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US-08-605-672-46
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US-08-605-672-46
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Best Local Similarity
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FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
APPLICATION NUMBER: 23-DEC-1993
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
TO ARDUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1155 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,67
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APPLICATION NUMBER: US
FILING DATE: 5-AUG-1994
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PRIOR APPLICATION NUMBER: US 08/362,652
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TYPE: amino acid
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: 2786
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5817515
                                    TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                               LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 121
                                                                                                                                                       PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
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TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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233 South Wacker Drive, 6300 Sear Tower
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28.2%; Pred. No. 6e-09;
43. Mismatches 96;
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Patent No. 5831029
                                                                                                                                                                                                                                                                                  Query Match
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SEQUENCE CHARACTERISTICS
LENGTH: 1155 amino ac
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US FILING DATE: 5-AUG-1994 PRIOR APPLICATION DATA:
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FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 08/173,497
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: No. 5831029el Human
NUMBER OF SEQUENCES: 103
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                                                                                                                                                                                                                                                 Local Similarity hes 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21-DEC-1994
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CLASSIFICATION:
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173 PVNDGFQALQGIIHSILKKSCIBILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
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                                  TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
                                                                    TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                        FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
                                                                                                                                                                           PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT
                                                                                                                                                                                                            PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 67
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3 South Wacker Drive, 6300 Sear Tower
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28.2%;
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Pred. No. 6e-09;
2; Mismatches
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Best Local (
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION US/08/947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                Local Similarity
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                                173 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
                                                                                                     122 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                                                        204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
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 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD
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TYPE: Floppy disk
                                                                     TDGQKFRDPLEYRHVIPEAEKA----GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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Pred. No. 6e-09;
42; Mismatches
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US-09-193-043-46
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                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6432404
GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 46
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
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EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/362,652
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
                                                                                                                           PRIOR APPLICATION NUMBER: 08/605,672
PRIOR FILING DATE: 1996-02-2
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
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APPLICATION
FILING DATE:
                                                            APPLICATION NUMBER: 08/362,652
                                                                                APPLICATION NUMBER: 08/286,889 FILING DATE: 1994-08-05
                                        FILING DATE: 1994-12-21
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o. 6251395
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                      08/943,363
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CURRENT APPLICATION NUMBER: US/09/350,259

CURRENT FILING DATE: 1999-07-08

EARLIER APPLICATION NUMBER: 09/193,043

EARLIER FILING DATE: 1998-11-16

EARLIER APPLICATION NUMBER: 08/173,497

EARLIER FILING DATE: 1993-12-23

EARLIER APPLICATION NUMBER: 08/286,889

EARLIER APPLICATION NUMBER: 08/286,889

EARLIER FILING DATE: 1994-08-05

EARLIER APPLICATION NUMBER: 08/382,652
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US-09-350-259-46
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-688-307A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 194-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mus musculus
-09-350-259-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
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Patent No. 6620915
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6600915el Human 2
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1155
                                                                                                                                                                                                                                                                                      Local
                                       122 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
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                                                                                  204 FTBFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
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                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                            LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIJAL 121
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TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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                                                                                                                                                                                                                                                           10.9%; Score 166; DB 4; I 28.2%; Pred. No. 6e-09; tive 42; Mismatches 96;
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Pred, No. 6e-09;
Pred, No. 6e-09;
Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485 617
FILING DATE:
CLASSIETT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 53, Application US/08485618 Patent No. 5728533
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
NAME: Williams Jr., JOSEPH A.
REGISTRATION UMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION UDATA:
APPLICATION UDBER: US 08/173,497
FILING DATE: 23-DEC-1993
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TITLE OF INVENTION: No. 5728533el Human
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                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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STATE: Illinois
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PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
                                                                        TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                              FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
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                                      TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF

    Marshall, O'Toole, Gerstein, Murray & Borun
    South Wacker Drive, 6300 Sear Tower

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Pred. No. 6e-09;
2; Mismatches 96
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316 KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSFQHEMSQEGFSSALSMD

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US-08-362-652-53
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
TITLE OF SECHIENCES: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312-474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States
ZIP: 60606-6402
MPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                              Local
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316
                                    173 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
                                                                            259
                                                                                                                 122 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                                                                                                                                                  144
                                                                                                                                                       204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
                                                                                                                                                                                          68 LTEDR----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIJAL 121
                                                                                                                                                                                                                                                                       10 PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK 67
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                                                                                                                                                                                                                                                                                                     h 10.9%; Score 166; DB 1; Lengtn Liv
Similarity 28.2%; Pred. No. 6e-09;
Mismatches 96; Indels
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KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD
                                                                                                                                                                                                                                  PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                            TDGQKFRDPLEYRHVIPEAEKA-
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    Marshall, O'Toole, Gerstein, Murray & Borun
    South Wacker Drive, 6300 Sear Tower

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SYSTEM: PC-DOS/MS-DOS
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RESULT 12

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US-08-482-293A-53; Sequence 53, Application US/08482293A
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                                     RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
APPLICATION NUMBER: US 08/362,652
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CITY: Chicago
Illinois
""nited
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
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TELEFAX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US (
FILING DATE: 5-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                              316
                                                                                                                               173 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
                                                                                                                                                                                                                                                 204 FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI 258
                                                                                                                                                                                                                                                                                                                         144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT
                                                                                                                                                                                                                                                                                    68 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 121
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66; Conserv
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                                                                                                                                                                                                           TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                                                                                                                                                                                                                                                                          PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK
                                                                                            KVGN-FVALRSIOROIQEK----IFAIEGTESRSSSFQHEMSQEGFSSALSMD 364
                                                                                                                                                                        TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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28.2%; Pred. No. 6e-09;
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APPLICANT:

Gallatin, W. Michael

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RESULT 14
US-08-943-363-53
; Sequence 53, Application US/08943363
; Patent No. 5837478
; Patent No. 58374770N;
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GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
APPLICANT: OF INVENTION: No. 5831029el Human
TTTMCES: 103
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/173,497
FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:
NUMBER: WILLIAM TERROR APPLICATION TO THE TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
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TELEPHONE: 314-4.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
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ZIP: 60606-6402
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STATE: Illinois
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                                                                                                                                             316
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                                                                                                                                                                                                                                                                                                                                                                                     144 PECPGQEMDIAPLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT 203
                                                                                                                                                                                                                                                                                                                                           68 LTEDR----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIJAL
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                                                                                                                                                                                                                       TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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233 South Wacker Drive, 6300 Sear Tower
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Pred. No. 6e-09;
12; Mismatches 96; Indels 3:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION UNMEER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
US 08/173,497
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 23-DEC-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 5-AUG-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5837478el NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 312-4.
                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                           122
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                                 173 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
                                                                                                                                                                                                                    144 PECPGQEMDIAFLIDGSGSIDQSDFTQMKDFVKALMGQLASTSTSFSLMQYSNILKTHFT
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KVGN-FVALRSIQRQIQEK----IFAIEGTESRSSSSFQHEMSQEGFSSALSMD 364
                                                                                                         TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF
                                                                                                                                            FTEFKSSLSPQSLVDAIVQLQ-----GLTYTASGIQKVVKELFHSKNGARKSAKKILIVI
                                                                                                                                                                                                                                                      PACYG-GFDLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMK
                                                                     TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
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233 South Wacker Drive, 6300 Sear Tower
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Pred. No. 6e-09;
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RESULT 15 US-09-193-043-53

Sequence 53, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica

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FILE OF INVENTION: NO. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
ENGLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTAL DATE: 1997-10-03
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTAL DATE: 2.0
SEQ ID NO 53
LENGTH: 1161
TYPE: PAT
ORGANISM: Mus musculus
US-09-193-043-53
Search completed: June 13, 2005, 20:05:08 Job time : 29.4879 secs
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                                                                                                                                                                                                                                                                               122 TDGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVF 172
                                                                                                                 316 KVGN-FVÁLRSÍQRQÍQEK----ÍFÁIEGTESRSSSFQHEMSQEGFSSÁLSMD 364
                                                                                                                                                                      173 PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVD 226
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                                                                                                                                                                                                                                259 TDGQKFRDPLEYRHVIPEAEKA---GIIRYAIGVGDAFREPTALQELNTIGSAPSQDHVF
                                                                                                                                                                                                                                                                                                                                                                         68 LTEDR-----EQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIAL 121
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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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DB seq length: 2000000000
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                                                                                                                              1526
                                                                                                                                                                                                                                                                                                                                                    is derived by analysis of the total score distribution
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Gapop 10.0 , Gapext 0.5
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1526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO9A_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO9A_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO9A_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO9A_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/USO9A_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB_pep:
/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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14
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  US-09-833-245-621

US-10-038-307-18

US-10-201-292-18

US-09-918-715-187

US-09-918-715-232

US-10-301-822-199

US-10-408-765A-1823

US-10-474-794-187

US-10-474-794-187

US-10-474-794-232

US-09-833-245-620

US-09-833-245-620
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Sequence 621, App
Sequence 18, Appl
Sequence 187, Appl
Sequence 187, App
Sequence 193, App
Sequence 193, App
Sequence 1823, App
Sequence 232, App
Sequence 232, App
Sequence 232, App
Sequence 620, App
Sequence 620, App
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4 <u>4</u>	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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50.7	•	•	•	•	•	59.2	•	•	•	•	•	96.9	•			•	•		•		•	•	•	٠	•	•	•	•	•	•	•	99.2	
587	488	488	488	488	488	538	460	460	479	504	529	534	534	543	543	543	543	543	543	342	342	328	328	562	562	562	562	564	564	345	345	333	333
9	15	14	14	14	10	13	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	16	16	10	10	14	14	14	14	14	14
US-09-764-870-312	-10-104-0	68-087-	-10-201-292-	-10-038-307-	-09-796-753-5	*	-10-201-292-3	92-2	2-3	01-292-3	-10-201-292-3	-10-201-292-	07-1	01-292-	-10-038-307-1	-10-201-292-1	-10-201-292-1	0-038-307-	-10-038-307-1	92-	-10-038-307-	US-10-201-292-26	0-038-307-2	US-10-474-794-301	-10-474-794-19	1	18-715-1	2	-10-038-307-2	-10-201-292-	38-307-	-10-201-29	38-307-
312, Ag	$\frac{\omega}{2}$	16	e 6, 1	equence 6,	equence 52,	equence 99,	equence 30,	equence 28,	32	34	36,	Sequence 12, Appl	12	10,	10,	16,	14, App	16,	14, App	e 22,	22, App	26,	e 26,	e 301,	e 194,	e 301,	e 194,	e 20,	е 2	24	e 24,	2, App	2

ALIGNMENTS

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621
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CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/29, 384
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-833-245-621
                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 621, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                    Matches
                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Albumin Pusion Proteins FILE REFERENCE: PF546PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Human Genome Sciences,
                                                                                                                                  293;
                     13
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RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGPERASEQIYYENRQGYRTASVIIA 120
                                                                              QGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST
                                                         QGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09833245 o. US20040010134A1
                                                                                                                                  100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                  0
                                                                                                                                  Score 1526; DB 11;
Pred. No. 1.1e-147;
; Mismatches 0;
                                                                                                                                                                     DB 11;
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                                                                                                                                                                     Length
                                                                                                                                                                       403;
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                                                                                                                                  Gaps
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RESULT 3
US-10-201-292-18
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SOFTWARE: FABTSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 551
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-18
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US-10-038-307-18
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Sequence 18, Application US/10201292

Publication No. US20030144193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: James B. ROTTWAN

APPLICANT: Theresa L. O'KBEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-299

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28
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Best Local Similarity
Matches 293; Conserv
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Publication No. US20030134786A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQA 180
                                                                                                                                                                                                                                                                                                                                            241 NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1526; DB 14;
100.0%; Pred. No. 1.8e-147;
htive 0; Mismatches 0;
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CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 18
LENGTH: 551
TYPE: PRT
ORGANISM: Homo sapien
US-10-201-292-18
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PAI
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT PILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: 60/24,360
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-01
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US-09-918-715-187
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                                                                                                                                                                                                                                                                LENGTH: 564
TYPE: PRT
ORGANISM: Homo Bapiens
US-09-918-715-187
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 187
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Publication No. US20030017157A1
                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                          61 RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA 120
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   LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQA 180
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                                   RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA 147
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                                                                                                                                                                                       100.0%; Score 1526; DB 10; 100.0%; Pred. No. 1.9e-147; vative 0; Mismatches 0;
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Pred. No. 1.8e-147;
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GENERAL INFORMATION:

APPLICANT: Brad St. Croix

APPLICANT: Bert Vogelstein

APPLICANT: Kenneth Kinzler

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00134

CURRENT APPLICATION NUMBER: 05/09/918,715

CURRENT FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/222,599

PRIOR FILING DATE: 2000-08-02

PRIOR FILING DATE: 2000-08-11

PRIOR FILING DATE: 2000-08-11

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR FILING DATE: 2000-08-11

PRIOR APPLICATION NUMBER: 60/282,850

PRIOR FILING DATE: 2000-04-11

NUMBER OF SEQ ID NOS: 358

SOPTWARE: PASTSEQ for Windows Version 3.0

SEQ ID NO 232

LENGTH: 564

TYPE: PRT
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US-10-301-822-199
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US-09-918-715-232
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                                                                                              Sequence 199, Application US/10301822 Publication No. US20030148410A1 GENERAL INFORMATION:
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Best Local
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APPLICANT: Miliennium Pharmaceuticals, APPLICANT: Berger, Allison APPLICANT: Guillemette, Tracy L. APPLICANT: Kamarkar, Shubhangi APPLICANT: Schlegel, Robert
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Sequence 1823, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Boin D.
APPLICANT: Tahy, Boin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1823
LENGTH: 564
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APPLICANT: Thibodeau, Stephen N.

APPLICANT: Burgart, Lawrence J.

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-029PZRNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/381,988
; TYPE: PRT ; ORGANISM: Homo sapiens US-10-408-765A-1823
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US-10-408-765A-1823
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NUMBER OF SEQ ID NOS: 228
SOPTWARE: FASTSEQ FOR WINDOWS Version 4.0
SEQ ID NO 199
LENGTH: 564
TYPE: PRT
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Length

564;

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PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR PELLOATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 187
LENGTH: 564
TYPE: PRT
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US-10-474-794-187
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US-10-474-794-187
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                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
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APPLICANT: St. Croix, Brad
APPLICANT: Vogelatein, Bert
APPLICANT: Kinzler, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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268
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                    NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG 293
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                                                                          LOGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL
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5. US20040213793A1
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Pred. No. 1.9e-147;
0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR PPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 620
LENGTH: 403
TYPE: PRT

RESULT 10 US-09-833-245-620

Sequence 620, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT

CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12

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APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PAY
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
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US-10-474-794-232
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Publication No. US20040213:
GENERAL INFORMATION:
APPLICANT: Carson-Walter,
APPLICANT: St. Croix, Br
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Best Local (
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 564
TYPE: PRT
ORGANISM: Homo sapiens
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                    241 NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG 293
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NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
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Vogelstein, Bert
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RESULT 11
US-09-796-753-12
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PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR PRILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR PILING DATE: 1998-12-30
PRIOR PILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR APPLICATION NUMBER: 09/345,536
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/345,164
PRIOR APPLICATION NUMBER: 09/345,164
PRIOR APPLICATION NUMBER: 09/345,164
PRIOR APPLICATION NUMBER: 09/345,164
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Publication No.
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CURRENT FILING DATE: 2001-03-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
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NAME/KEY: SITE
LOCATION: (368)
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LOCATION: (331)
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LOCATION: (320)
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Similarity 99.7%;
91; Conservative
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Pred. No. 1.5e-146;
0; Mismatches 1;
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RESULT 12 US-10-038-307-2

Sequence 2, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
APPLICANT: TRENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999

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; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
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PRIOR FILING DATE: 20
NUMBER OF SEQ ID NOS:
SEQ ID NO 12
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Best Local Similarity
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APPLICATION NUMBER: 09/4
FILING DATE: 1999-12-29
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FILING DATE: 2000-09-30
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FILING DATE: 2000-09-20
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APPLICATION NUMBER: 09/474,071
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NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCS
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                                                                                                                     LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQA
                                                             LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL
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CURRENT APPLICATION NUMBER: US/10/038,307; CURRENT FILING DATE: 2002-06-28; NUMBER OF SEQ ID NOS: 26; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 2; ELENGTH: 333; TYPE: PRT; ORGANISM: Homo Bapiens
US-10-038-307-2
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APPLICANT: Theresa L. O'KEEPE
APPLICANT: Engin OZKAYNAK
APPLICANT: JUdith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Core FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILLING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-201-292-2
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Publication No. US20030144193A1
                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: Homo sapiens
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LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL
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100.0%; Pred. No. 1.5e-146;
tive 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 24
LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-24
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US-10-038-307-24
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US-10-201-292-24
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                                                  GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT PILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 Sequence 24, Application US/10201292
Publication No. US20030144193A1
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Publication No. US20030134786A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KERFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-2959
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
LENGTH: 345
TYPE: PRT
ORGANISM: Homo
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   sapiens
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Pred. No. 1.6e-146;
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US-10-201-292-24	-292-24
Query Match Best Local	tch 99.2%; Score 1514; DB 14; Length 345; al Similarity 100.0%; Pred. No. 1.6e-146;
Matches	Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
δ.	1 QGGRREDGGPACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST 60
Вb	28 QGGRREDGGPACYGGPDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFST 87
ફ	61 RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA 120
망	88 RGTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA 147
Ş	121 LTDGELHEDLFFYSEREAURSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQA 180
B	148 LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQA 207
δ	181 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL 240
B	208 LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL 267
ş	241 NEKPPSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCS 291
98	268 NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTHCS 318
Search com Job time :	Search completed: June 13, 2005, 20:36:50 Job time : 94.9469 secs

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Copyright
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 13, 2005, 19:47:08 ; Search time 21.0213 Seconds (without alignments) 1341.095 Million cell updates/sec

Perfect score: Title: US-09-970-076-2_COPY_28_320 1526

Sequence: 1 QGGRREDGGPACYGGFDLYF.....DGLSFISSSVIITTTHCSDG 293

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched

Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Maximum Minimum B B seq length: 0
seq length: 2000000000

Post-processing:

Minimum Match 0% Maximum Match 100 Listing first 45 100% gummaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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collagen alpha 3 (V dnaK protein NMB05 collagen alpha 3 (V hypothetical proteintegrin alpha-1 - probable retroelem transcription reguinter-alpha-inhibi integrin alpha-E cintegrin alpha-E cintegrin alpha-E cintegrin alpha-E cundulin 1 - human hypothetical proteprobable chaperone transposase (04) B	hypothetical prote

ALIGNMENTS

cell surface glycoprotein CD11b precursor [validated] - human
N,Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Ma
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text change 09-Jul-2004
C;Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD

A;Reference number: A31108; MUID:88315033; PMID:2457584

A;Accession: A31108
A;Accession: A71108
A;Molecule type: mRNA
A;Residues: 1-1153 <COR>
A;COBS-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A;COBS-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A;Note: part of this sequence was confirmed by protein sequencing
A;Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
J. Cell Biol. 106, 2153-2158, 1988
A;Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor M:
A;Reference number: A28915; MUID:88257215; PMID:2454931
A;Accession: A28915

A;Molecule type: mRNA
A;Residues: 1-499,501-965,'P',967-1153 <ARN>
A;Residues: 1-499,501-965,'P',967-1153 <ARN>
A;Residues: Teres: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594:
A;Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594:
A;Cross-references: GB:M18044; GB:J03270; GB:M19664; GB:X07421; NID:g186935; PIDN:AAA594:
A;Note: the authors translated the codon TAC for residue 1129 as Thr
A;Note: part of this sequence, including the amino end of the mature protein, was confir.
A;Note: part of this sequence, including the amino end of the mature protein, was confir.
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A; Molecule type: DNA A; Residues: 1-9 < SHE>

A;Cross-references: GB:M76724; NID:g180018; PIDN:AAA58410.1; PID:g553215 R;Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris, P.; Tenen, D.G. Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988 A;Title: Molecular cloning of the alpha-subunit of human and guinea pig leuk A;Reference number: A94193; MUID:88190151; PMID:2833753

guinea pig leukocyte adhesic

A; Accession: A30892

A; Molecule type: mRNA A; Residues: 917-1042 < AR2>

A;Cross-references: GB:M18044
R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: cDNA sequence for the alpham subunit of the human neutrophil adherence receptor A;Reference number: A32218, MUID:89098893; PMID:2563162
A;Accession: A32218

A; Molecule type: mRNA

9-1153 <HIC>

A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975

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A;Map position: 16p11.2-16p11.2

A;Map position: 16p11.2-16p11.2

A;Note: promoter contains a GATA motif and two Spl consensus binding sites
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home
C;Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; mag
F;1-16/Domain: signal sequence #status predicted <SIG>
F;1-118/Domain: signal sequence #status predicted <EXT>
F;17-119/Domain: extracellular #status predicted <EXT>
F;148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F;146-433/Region: calcium/magnesium binding #status predicted
F;330-538/Region: calcium/magnesium binding #status predicted
F;533-601/Region: calcium/magnesium binding #status predicted
F;533-601/Region: calcium/magnesium binding #status predicted
F;1109-1134/Domain: transmembrane #status predicted <TMM>
F;1135-Domain: intracellular #status predicted <TMM>
F;1135-Domain: transmembrane #status predicted <TMM>
F;1135-Domain: transmembrane #status predicted <TMM>
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F;105-Domain: transmembrane #sta
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R;Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
A;Title: Characterization of the myeloid-specific CD11b promoter.
A;Reference number: IS2567; MUID:92144986; PMID:1346576
A;Accession: IS2567
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A;Note: the last three bases of intron 13, CAG, are included in some but not all matur A;Note: sequence extracted from NCBI backbone (NCBIP:121963)
R;Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
Biochim. Biophys. Acta 874, 368-371, 1986
A;Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across A;Reference number: A90664; MUID:87076671; PMID:3539202
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A; Residues: 1-9 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                VNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTFKEFQNNPNFRSLVKPITQLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR-----IADS--KDHVPP 173
                                                                                                                                                                                                                                                                                                                                                                   DGEKFGDPLGYEDVIPEADRE---GVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 122
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26.2%; Pred. No. 0.0016;
tive 45; Mismatches 8
    precursor -
                                                                                                                                                                                                          IFAIEGTQTGSSSSFEHEMSQEGFSAA
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N;Alternate names: fibrochimerin
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #Bequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811
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                                                                                                                                                                 collagen alpha 1(XII) chain precursor -
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A;Map position: 16p11.2-16p11.2

G;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol C;Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat; F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>
F;20-1107/Domain: extracellular #status predicted <ATNP
F;149-319/Domain: von Willebrand factor type A repeat homology <VWA4>
F;1108-1133/Domain: transmembrane #status predicted <INT>
F;1134-1163/Domain: intracellular #status predicted <INT>
F;61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: this sequence has been revised in reference A36584 R;Corbi, A.L.; Miller, L.J.; O'Connor, K.; Larson, R.S.; Spi EMBO J. 6, 4023-4028, 1987 A;Title: cDNA cloning and complete primary structure of the A;Reference number: S00864; MUID:88166645; PMID:3327687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:119758; OMIM:151510
A;Cross-references: GDB:119758; OMIM:151510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA, A;Molecule type: mRNA, A;Molecule type: mRNA, A;Residues: 1-755,'L',757-1163 <CO3>
A;Residues: 1-755,'L',757-1163 <CO3>
A;Cross-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A;Note: part of this sequence was confirmed by protein sequencing
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: this revision to the sequence from reference A35543 includes R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A;Title: Genomic structure of an integrin alpha subunit, the leukocyta;Reference number: A35543; MUID:90153906; PMID:2303426
A;Accession: A35543
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A;Residues: 1-1163 <COR>
A;Cross-references: UNIPROT:P20702
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A;Contents: erratum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
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A; Residues: 1-834 <CO2>
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                                                                           SLDYKD-VIPMADAAGIIRYAIGVGLAFQNRNSWKELND----IASKPSQEHIFKVED-
                                                                                                                                                                                                             NPLSLLASVHQLQ-----GFTYTATAIQNVVHRLFHASYGARRDATKILIVITDGKKEGD
                                                                                                                                                                                                                                                                                  ---QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTAS-VIIALTDGELHED
                                                                                                                                                                                                                                                                                                                                                       DIVELIDGSGSISSRNFATWANIEQFQRPSTQFSLMQFSNKFQTHFTFEEFRRTS
                                                                                                                                                                                                                                                                                                                                                                                                                        DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE--
FOALQGIIHSILKKSCIEILAAEPSTICAGESFOVVVRGNGF
                                                                                                                                         LFFYSEREANRSRDLGAIVYCVGV------KDFNETQLARIAD--SKDHVFPVNDG 177
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R;Dublet, B.; van der Kubl, ...
J. Biol. Chem. 262, 17724-17727, 1987
J. Riol. Chem. 262, 17724-17727, 1987
A;Title: Type XII collagen is expressed in embryonic chick tendons.
A;Reference number: $22254; MUID:88087065; PMID:3121603
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A;Title: A major oligomeric fibroblast proteoglycan identified A;Reference number: S23814; MUID:92362621; PMID:1323460
A;Accession: S23814
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Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A/Title: Type XII collagen: distinct extracellular matrix
A/Reference number: A28037; MUID:87317590; PMID:3476925
A/Accession: A28037
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A;Title: Type XII collagen. A large multidomain molecule with partial homology to A;Reference number: A34485; MUID:90062079; PMID:2584192
A;Accession: A34485
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A;Residues: 1-3124 <YAM>
A;Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PIA;Cross-references: UNIPROTOS PIDN:BAA00701.1; PIA;Cross-references: UNIPROTOS PIDN:BAA00701.1; PIA;Cross-references: UNIPROTOS PIDN:BAA00701.1; PIA;Cross-references: UNIPROTOS PIDN:BAA00701.1; PIA;Cross-references: UNIPROTOS PIDN:BAA00701.1; PIA;Cross-references: UNIPROTOS PIDN:BAA00701.1; PIA;Cross-references: UNIPROTOS PIDN:BAA00701.1; PIA;Cross-references: UNIPROTOS PIDN:BAA00701.1; PIA;Cross-references: UNIPROTIS PIDN:BAA00701.1; PIA;Cross-refere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1171, 97-98, 1992
A;Title: The two splice variants of collagen XII share a
A;Reference number: S28811; MUID:93042014; PMID:1420368
A;Accession: S28811
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A;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
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A,Residues: 2960-2976,'F',2978-3074,'AG' <GOR3>
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A; Residues: 2772-2792; 2846-2873 <GOR2>
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,Residues: 'X',133,'Q',1335-1347,1914-1928,2504,'X',2506,'X',2508-2511,'X',2513-2517
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factor type A repeat homology
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A;Molecule type: DNA
A;Residues: 1-1153 <PYT>
A;Residues: 1-1153 <PYT>
A;Residues: 1-1153 <PYT>
A;Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983
A;Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983
A;Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983
A;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A;Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept A;Reference number: 159078; MUID:86287312; PMID:2942940
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A; Title: Amino acid sequence of the murine Mac-1 alpha chain A; Reference number: S00551; MUID:88312584; PMID:3044779
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A;Cross-references: GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193
                   A; Molecule type: DNA
A; Residues: 11-44 < RES>
                                                                                        A; Accession:
                                                                                                                                                                                                                                                                                                    A; Accession: S00551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukocyte surface glycoprotein Mac-1 alpha chain precursor
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F;1655-1738/Domain:
                                                               Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                          ;Date: 30-Sep-1989 #sequence_revision;Accession: S00551; I59078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternate names: complement-3 receptor alpha chain (Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;1847-1928/Domain:
;1937-2019/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF---KEPAIKLRDADVEIFAVGVKDAVRTELEAIASPPAETHVYTVED-FDAFQRISFE 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NRVKDIIQAINTFPYRGGSTNTGKAMTYVREKVFVTSK-GSRPNVPRVMILITDGK-SSD
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fibronectin type III repeat homology <FN3I>
fibronectin type III repeat homology <FN3K-
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fibronectin type III repeat homology <FN3N-
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fibronectin type III repeat homology <FN3N-
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26.1%; Pred. No. 0.0097;
71. Mismatches 97;
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A;Gene: Mac-1
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homo C;Superfamily: cell surface glycoprotein; transmembrane protein C;Keywords: cell adhesion; glycoprotein; transmembrane protein F;1-16/Domain: signal sequence #status predicted <SIG> F;1-16/Domain: signal sequence #status predicted of alpha chain #status experimental F;17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status experimental F;148-318/Domain: von Willebrand factor type A repeat homology <VWA2> F;1106-1129/Domain: transmembrane #status predicted <TWM>
                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q04588; GB:M99058; NID:g158890; PID:g158891
A;Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)
F;45-218/Domain: von Willebrand factor type A repeat homology <TWA2>
F;238-296/Domain: thrombospondin type 1 repeat homology <TWR1>
F;309-371/Domain: thrombospondin type 1 repeat homology <TWR3>
F;372-432/Domain: thrombospondin type 1 repeat homology <TWR3>
F;431-432/Domain: thrombospondin type 1 repeat homology <TWR4>
F;474-556/Domain: thrombospondin type 1 repeat homology <TWR4>
F;494-556/Domain: thrombospondin type 1 repeat homology <TWR6>
F;4960-610/Domain: thrombospondin type 1 repeat homology <TWR6>
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Mol. Biochem. Parasitol. 57, 11-714, 1993
A;Title: Sequence of a major Eimeria maxima antigen homologous
A;Reference number: A48569; MUID:93149203; PMID:8426611
A;Accession: A48569
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C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A48569
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A; Residues: 1-724 < PAS>
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                                             ELHEDLFFYSERE-----ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP- 173
                                                                                                  SDSRAQNADLLAAAAKKLPYAAGSTYTHLGLAKA-EEILFSFQKGGRDNAPKMILVMTDG
                                                                                                                                                  TEDREQIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDG
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SSRRSQTLSAAEKLKNRGVÍ I VVLGVGTGVNSAECRSÍ AGCDTSDTVECFR
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24.2%; Pred. No. 0.0038;
htive 50; Mismatches 96
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                                                                                                                                                                                                                                                                                                       Score 139; DB 2
Pred. No. 0.003;
0; Mismatches
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A;Molecule type: protein
A;Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
A;Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime: r;40-204/Domain: von Willebrand factor type A repeat homology <FN3A>
r;326-317/Domain: fibronectin type III repeat homology <FN3B>
r;326-409/Domain: fibronectin type III repeat homology <FN3C>
r;418-498/Domain: fibronectin type III repeat homology <FN3D>
r;507-591/Domain: fibronectin type III repeat homology <FN3B>
r;625-707/Domain: fibronectin type III repeat homology <FN3F>
r;625-707/Domain: fibronectin type III repeat homology <FN3G>
r;706-798/Domain: fibronectin type III repeat homology <FN3G>
r;924-1089/Domain: fibronectin type III repeat homology <FN3G>
r;924-1089/Domain: von Willebrand factor type A repeat homology <VWA2>
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A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: A45974; S30085; S22916; S17035; S20833 R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, J. Biol. Chem. 268, 12177-12184, 1993 A;Title: Type XIV collagen is encoded by alternative transcripts with distinct 5'
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C;Species: Gallus gallus '
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A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)
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Eur. J. Biochem. 20
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A; Residues: 1472-1660 < APT>
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A; Residues: 1-1747 < GER >
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A, Residues: 1472-1659 <GOR1>
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                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                    926
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                                                                                                         DLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGFDGTQVAIIQFSDDFRTEFKLNAYK 985
    DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 128
                                                                                                                                                                                     DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 70
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                                                                                                                                                                                                                                                                                Score 137; DB 2;
Pred. No. 0.014;
5; Mismatches 114
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N;Alternate names: C3 convertase; C5 convertase; complement C2 (Specias: Mus musculus (house mouse) C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change C;Accession: A38876; B36593; T54429 R;Ishikawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, H.R. submitted to GenBank, January 1991
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A45638
A; Reference number: A38875
A; Accession: A38876
                                                                                                                                                                   classical-complement-pathway C3/C5 convertase (EC 3.4.21.43)
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A;Title: Sequence of the gene encoding an immunodominant microneme A;Reference number: A45638; MUID:92131064; PMID:1775171
A;Accession: A45638
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C/Species: Eimeria tenella
C/Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;MOICUle type: DNA;
;Residues: 1-712 <TOM>
;Residues: 1-712 <TOM>
;Cross-references: UNIPROT:043981; GB:AF032905; GB:M73495; NID:g2707732; PIDN:AAD03350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,433-493/Domain: thrombospondin
,494-556/Domain: thrombospondin
,560-610/Domain: thrombospondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                     P-----VNDGFQALQGIIHSILKKSCIEILAAEPSTI--CAGE
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                                                                                                                                                                                                                                                                           PRYLOSNWSNVTQQVNGII KAACKDLAKDAVCSEWSEYGPCVGE
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Pred. No. 0.00
40; Mismatches
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                                                                                                                                                                                                                                                                                                                     208
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                                                                                                        09-Jul-2004
                                                                                                                                                                   component precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113
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F;1-18/Domain: signal sequence #status predicted <SIGs
F;19-250/Product: complement C2b fragment #status predicted <C2Bs
F;22-89/Domain: complement factor H repeat homology <FH12s
F;94-149/Domain: complement factor H repeat homology <FH2s
F;156-210/Domain: complement factor H repeat homology <FH3s
F;251-760/Product: complement C2a fragment long form #status predicted <C2As
F;251-7605,613-760/Product: complement C2a fragment short form #status predicted <C2As
F;259-449/Domain: von Willebrand factor type A repeat homology <VFAs
F;259-449/Domain: typsin homology #status atypical <TRYs
F;478-747/Domain: trypsin homology #status atypical <TRYs
F;478-747/Domain: trypsin homology #status atypical <TRYs
F;27-62,49-89,94-136,122-149,156-197,182-210,470-590,499-515,593-609,647-674,685-715/Disu
F;27,117,297,340,474,778,663/Binding site: carbohydrate (Asn) (covalent) #status predicte
F;514,570,689/Active site: His, Asp, Ser #status predicted
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C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; vc

C;Keywords: alternative splicing; complement classical pathway; duplication; glycoproteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 16/1; 91/1; 153/1; 212/1; 245/3; 290/3; 337/1; 384/1; 414/1; 461/1; C;Complex: The proenzyme forms a complex with C4a and is activated by cleavage C;Function:
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A;Residues: 1-760 <IS2>
A;Cross-references: UNIPROT:P21180; GB:M57891; GB:J05661; NID:g192436; PIDN:AAA63294.1;
R;Ishikawa, N.; Nonaka, M.; Wettel, R.A.; Colten, H.R.
J. Biol. Chem. 265, 19040-19046, 1990
A;Title: Murine complement C2 and factor B genomic and cDNA cloning reveals different me A;Reference number: A36593; MUID:91035430; PMID:2229060
A;Accession: B36593.
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A;Cross_references: GB:M16271; NID:g199289; PIDN:AAA39562.1; PID:g199290
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A;Residues: 1-760 <ISH>
A;Cross-references: RBL:M57891; NID:g192436;
R;Falus A; Wakeland, B.K.; McConnell, T.J.;
Immunogenetics 25, 290-298, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: cleaves complement C3 and complement C5 alpha chains
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A; Residues: 660-677,'I
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Best Local
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                                                            MND-----GLSFISSSVII 285
                                                                                                                                                                                    GNGFRHARNVDRV--LCSFKINDSVTLNEKPFSVEDTYLLCPAPILKEVGMK--AALQVS
                                                                                                                                                                                                                                                                                                      FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGESFQVVVR
                                                                                                                                                                                                                                                                                                                                                                   KEIRHTIILLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDDYLDIYAIGVGKLDVDWKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GHLNLYLLLDASQSVTEKDFDIFKKSAELMVERIFSFEVNVTVAIITFASQPKTIMSILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGFDLYFILDKSGSVLHHWNBIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTE 70
VGDPTSQHGKEFLVEDVII
                                                                                                                     GNMSANASDQERTPWQVTFKPKSKETCQGS--LISDQWVLTAAHCFHDIQMEDHHLWRVN
                                                                                                                                                                                                                                          LNE--LGSKKDGERHAFILQDA-KALQQIFEHMLDVSKL-
                                                                                                                                                                                                                                                                                                                                                                                                                               ----VIIALTDGELHEDLFFYSEREANRSRDLGAI-----VYCVGV------KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERSO-----DVTEVITSLDSASYKDHENATGANTYEVLIRVYSMMQTQMDRLGMETSAW 371
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Pred. No. 0.014;
6; Mismatches 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115;
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into C2a,
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RESULT 9
\$31212
collagen alpha 1(XIV) chain precursor,
C;Species: Gallus gallus (chicken)

short

form

chicken

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A;Residues: 1-1888 <TRUS
A;Cross-references: UNIPROT: P32018; EMBL: X70793; NID: 9288872; PIDN: CAA50064.1;
R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID: 93185668; PMID: 8444186
A;Accession: S31211
A;Status: preliminary
A;Molecule type: mRNA
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S78476
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F;442-525/Domain: fibronectin type III repeat homology <FN3C>
F;534-614/Domain: fibronectin type III repeat homology <FN3C>
F;623-707/Domain: fibronectin type III repeat homology <FN3E>
F;741-923/Domain: fibronectin type III repeat homology <FN3F>
F;731-923/Domain: fibronectin type III repeat homology <FN3G>
F;932-1009/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3G>
                                                                                                                                                                                                                                                                          A; Reference number: $78476
A; Accession: $78476
                                                                                                                                                                                                                                                                                                                                                                                collagen alpha 1(XIV) chain precursor, long form - C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998
C;Accession: S78476; S31211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Complete primary structure of chicken collagen XIV A;Reference number: S31211; MUID:93185668; PMID:8444186 A;Accession: S31212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Waelchli,
                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, January 1993
                                                                                                                                                                                                                                                                                                                                                            R, Trueb,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: Coll4A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Keywords: alternative splicing; coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession:
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J. Biochem. 212, 483-490,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1213 DELITFVCETASATCPLVFKDGDKLA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE
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larity 25.0%; Pred. No. 0.055;
Conservative 44; Mismatches 116; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GPKMMEMFGLVEKEFSAIDGVSMEPGTF 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        extracellular matrix; glycoprotein;
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A,Residues: 1-416;1460-1811,1843-1888
A,Cross-references: EMBL:X70793
C;Genetics:
                                                                                                                                                                                                          F;512-679/Domain: von Willebrand factor type A repeat homology <VWA1>F;754-793/Domain: fibronectin type II repeat homology <2F1>F;1201-1244/Domain: EGF homology <EGF>
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A; Residues: 1-3051 <SMI>
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                                                                                                                                                                                                                                                                                                                                                                                                        R;Smith, A
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                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z30423; NID:g458479; PID:g458485
                                                                                                                                                                                                                                                                                                                                                       A;Accession: S42373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T20G5.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1040-1205/Domain:
                                                                                                                                                                                                                                                                                 ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: S42373
                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Caenorhabditis elegans;
Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004;
                                                                                                                                                         Query Match
Best Local Similarity
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                                    44
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ELFEIGRSKTRVGLIQYSDQIRHEFDLDQYGDRDSLLKGISETQ-YLTGLTRTGAAIQHM
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                                                                                                         CYGGF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E
                                  HKFI--SPQLRMSFIVFSTRGTTLMKLTE--DREQIRQGLEELQKVLPG----GDTYMH-
                                                                   CYGGFVDVSSNANLPPGRVCTVQTTCPKQKTDLVFLIDGSGSIGSYVFKNEVLRFVREFV
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                                                                                                                                        Conservative
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                                                                                                                                       8.4%; Score 128; DB 2; Length 3051;
27.1%; Pred. No. 0.15;
tive 31; Mismatches 75; Indels 6
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factor type A repeat homology
                                                                                                                                                                                                                                                                                                                                                                                          March
                                                                                                        ------DLYFILDKSGSVLHH--WNEIYYFVEQLA 43
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R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, J. Biol. Chem. 265, 19624-19631, 1990
A;Title: Structure and chromosomal location of the
A;Molecule type: mRNA
A;Residues: 157-290,'L',292-496 <JE2>
A;Cross-references: GB:M55883; GB:J05666;
                                                                                                                                                                                                                                                                                         cartilage matrix protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004
C;Accession: A37979; B37979
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A;Title: Monoclonal antibody MT2 identifies the urodele A;Reference number: 151027; MUID:95246925; PMID:7729585
A;Accession: I51027
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                                                                                                                            A, Residues: 1-496 <JEN>
                                                                                                                                                                        A;Reference number: A37979;
A;Accession: A37979
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                                                                              A, Accession: B37979
                                                                                                    A, Cross-references: UNIPROT: P21941; GB:J05667
                                                                                                                                                A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-references: UNIPROT:Q91145; EMBL:U19494; NID:g632647; PIDN:AAA80217.1; PID:g6326;155-236/Domain: fibronectin type III repeat homology <3FR>;631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Residues: 1-929 <WEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVN-DGFQALQGIIHSI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 LKKSCIEILAA----EPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  693 KKSLMDAVANLPYKGGNTNTGSALKFILENNF---RPGVGMREKARKIAILLTDGKSQDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSVEDTYLLCPAPILKEVGMKAALQVSMN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIVLLVDGSWSIGRPNFKIVRNFISRVVEVFDIGSDRVQIAVSQYSGDPRTEWQLNTHKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TENVCNSVKGPGGLNPPSNLVTSEPTPRSFRVTWVPPSQSVER----FKVEYYPVAGGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVAPSKRYA----DEGIELYAVGIKNADENELKETASDPDELYMYNVADPSLLTNIVNDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQGLEELQKVLP---GGDTYMHEGFERASEQIYYENRQGY----RTASVIIALTDGELHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TFAIGVTDHVLASELESIAGSPNRWFYV-DKFKDLDTRLRSMIQK-----AACPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYCVGVKD-FNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIEILAAEPS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQEGF-----SERRGARPQQSDIARVAIILTDGRSQDNV----TGPADSARKLSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --EGFERASEQIYYENRQGYR-----TASVIIALTDGELHEDLFFYSEREANRSRDLGAI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QEVYVRGTQTTTVLVGLKPETEYYVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E.V.; Klatt, K.P.; Tassava, R.A.
                                                                                                                                                                                              chromosomal location of the human gene encoding cartilage matrix 1979; MUID:91060568; PMID:2246248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.7%; Score 118; DB 2; Length 929; 21.2%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
       GB:J05667; NID:g180651; PIDN:AAA63904.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135;
                                                                                                                                                                                                                                                                   A.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                   Jr., R.L.; Byers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
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                                                                                                                                                                                                                                                              M.G.;
       PID:
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A;Note: glycosylation sites were R;Christie, D.L.; Gagnon, J. Biochem. J. 209, 61-70, 1983
                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 467-546;550-595;752-764 <MOO>
A;Residues: 467-546;550-595;752-764 <MOO>
A;Cross-references: GB:J00185; GB:J00186
A;Note: the authors translated the codon TAC at 519 as Thr; t
A;Nole; J.B.; Anderson, J.K.; Davison, E.A.; Woods, D.E.
Chem. 259, 3407-3412, 1984
A;Title: Complete primary structure for the zymogen of human
A;Reference number: A20751; MUID:84161997; PMID:6546754
A;Accession: A00934
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P00751; EMBL:X72875; NID:g297568; PIDN:CAA51389.1; R;Woods, D.E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, H.R. Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982
A;Title: Isolation of cDNA clones for the human complement protein factor B, a A;Reference number: A44622; MUID:83039428; PMID:6957884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:127280; OMIM:115437
A;Map position: 1p35-1p35
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
C;Complex: homotrimer
                                                                           A;Note: nucleic acid translation differs from A;Note: 736-Ser was also found
                                                                                                                                                 A; Molecule type: protein; mRNA
A; Residues: 26-764 < MOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data A; Reference number: S34075 A; Accession: S34075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-764 < ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         몽
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                                                                                                                              A;Cross-references: GB:K01566
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: A44622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Mejia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement factor B precursor [validated] - human
N;Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; heat-l
N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;76,344/Binding site: carbohydrate (Asn) (covalent) #status F;221-238,234-247,249-262/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;273-437/Domain: von Willebrand factor type A repeat homology <VWA2> F;76,344/Binding site: carbohydrate (Asn) (covalent) \#8tatus predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1-22/Domain: signal sequence #status predicted <SIG>F;23-496/Product: cartilage matrix protein #status predicted <MAT>F;33-206/Domain: von willabrand factor type A repeat homology <VWAl>F;33-206/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: cartilage matrix protein; EGF homology; von
C;Keywords: glycoprotein; homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 QEFPLGRFHTKKDIKAAVRNM------SYMEKGTMTGAALKYLIDNSFTVSSGARPGA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 CYGG-----FDLYFILDKSGSVL-HHWNEIYYFVEQLAHKF-ISPQLRMSFIV---FSTR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-764 <MEJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY----YENRQGYRTAS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTAD-FKTINQIGKKLQKKICVE---EDP---CACESLVKFQAKVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVNDGFQALQGIIHSILKKSCIEILAAEPSTICAGES---FQVVVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKVGIVFTDGRSQD----YINDAAKKAKDLGFKMFAVGVGNAVEDELREIASEPVAEHYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --VIIALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADS--KDHVF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSGGGGSSATDLVFLIDGSKSVRPENFELVKKFISQIVDTLDVSDKLAQVGLVQYSSSVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 113.5;
Pred. No. 0.21
35; Mismatches
                                                   determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. 0.21;
                                                                                                   the
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                                                                                                   sequence
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                                                                                                                                                                                                                                                                                                                                     nucleic acid translation
                                                                                                   Ħ
                                                                                                having
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                                                                                                                                                                                                                                                          factor B
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                                                                                                   300-Leu,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID: 929756
                                                                                                   328-1
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Amino acid sequence

of the

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fragment

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complement

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Sequence

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A; Map position: 6921.3-6921.3
A; Map position: 8921.3-6921.3
A; Map position: 8931.3-6921.3
A; Map position: 8931.3-6921.3
A; Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3;
A; Note: the list of introns may be incomplete
A; Note: gene is located in the major histocompatibility complex, class III region
C; Complex: complement factor B initially forms an inactive complex with complement fac ment factor C3b forming active C3/C5 convertase; Ba is released
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 270-329 «NIB»
A;Residues: 210-329 «NIB»
A;Rote: binding site for carbohydrate to lysine under artificial conditions
R;Morley, B.J.; Campbell, R.D.
EMBO J. 3, 153-157, 1984
A;Title: Internal homologies of the Ba fragment from human complement component
A;Reference number: A44628; MUID:84158524; PMID:6323161
A;Accession: A44628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; MOJecule type: mRNA
A; Residues: 339-509 <Al>
A; Residues: 339-509 <Al>
A; CROSS-references: GB:J00126; NID:g187723; PIDN:AAA36226.1;
A; Wu, L.; Morley, B.J.; Campbell, R.D.
Cell 48, 331-342, 1987
A; Title: Cell-specific expression of the human complement pro
A; Reference number: A25971; MUID:87102880; PMID:3643061
A; Accession: B25971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; PID:g4261689 R;Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, S.; Volanak Mol. Immunol. 30, 1587-1592, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Campbell, R.D.; Porter, R.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983
A;Title: Molecular cloning and characterization of the gene A;Reference number: A19947; MUID:83273641; PMID:6308626
A;Accession: A19947
A; Pathway:
                                                                  A;Description: Bb is a serine proteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-31,'Q',33-764 <RE2>
A;Cross-references: GB:L15702; NID:g291921; PIDN:AAA16820.1;
C;Comment: 292-Cys has a free sulfhydryl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic conv
A;Reference number: I57824; MUID:94067177; PMID:8247029
A;Accession: I57824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-764 < RES>
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A;Accession: I54409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 16-225, 'F.,27-259 <MOR>
R;Schwaeble, W.; Luttig, B.; Sokolow
Immunobiology 188, 221-232, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: S14339; MUID:91174758; A;Accession: S14339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. J. 274, 473-480, 1991
A; Title: The principal site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-99 < WUL>
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A;Residues: 346-764 <CAM>
A;Crose-references: GB:J00125
A;Accession: B19947
                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:119726; OMIM:138470
                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Human complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Niemann, M.A.; Bhown, A.S.; Miller,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M15082; NID:g187699; PIDN:AAA59625.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Accession: A19188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Reference number: A19188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
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9; MUID:94041399; PMID:8225386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUID:83204002; PMID:6342610 in a series documenting the sequence, glycosylation site,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of glycation of human complement
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                                                                  convertase cleaves complement C3
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C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; vc C;Roywords: acute phase; complement alternate pathway; duplication; glycoprotein; hydrolf F;1-25/Domain: stignal sequence #status predicted cSIG>
F;26-764/Product: complement factor B #status experimental <MAT>
F;26-259/Product: complement factor B #status experimental <MAT>
F;37-98/Domain: complement factor B #status experimental <BAF>
F;103-158/Domain: complement factor H repeat homology <FH2>
F;105-218/Domain: complement factor H repeat homology <FH2>
F;260-764/Product: C3/C5 convertase Bb fragment #status experimental <BBF>
F;260-764/Product: C3/C5 convertase Bb fragment #status experimental <BBF>
F;482-752/Domain: trypsin homology #status atypical <TRY>
F;37-76,62-98,103-145,131-158,165-205,191-218,478-596,511-527,599-615,656-682,695-725/Dif
F;122,142,285,378/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;259-260/Cleavage site: Arg-Lys (complement factor D) #status experimental
F;572,576,699/Active site: His, Asp, Ser #status experimental
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A54849
                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-2944 < CHR>
A;Residues: 1-2944 < CHR>
A;CTOSS-references: UNIPROT:Q02388; GB:L02870; NID:g987124; PIDN:AAA7
A;CTOSS-references: UNIPROT:Q02388; GB:L02870; NID:g987124; PIDN:AAA7
R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
Biochem. Biophys. Res. Commun. 183, 958-963, 1992
A;Title: Molecular cloning and characterization of type VII collagen
A;Reference number: PH0844; MUID:92231902; PMID:1567409
A;Accession: PH0844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text change 09-Jul-2004 C;Accession: A54849; PH0844; S16316; I56328; A30296; I84686 R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J. Biol. Chem. 269, 20256-20262, 1994 J. Biol. Chem. 269, 20256-20262, 1994 A;Title: Cloning of human type VII collagen. Complete primary sequence of the A;Reference number: A54849; MUID:94327588; PMID:8051117
                                                                                    A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 'EFR',340-475,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,'C',
A;Residues: DBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:BAA02853.1; PID:g453699
A;Experimental source: keratinocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(VII) chain precursor - human
N;Alternate names: procollagen alpha 1(VII) chain
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                                A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr R:Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Baue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  뭉
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R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A54849
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19.6%; Pred. No. 0.37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVVSEYFVLTAAHC
   Woodley, D.T.;
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F;36-201/Domain: von Willebrand factor type A repeat homology <PWA1>
F;231-318/Domain: fibronectin type III repeat homology <PRI>
F;237-413/Domain: fibronectin type III repeat homology <PRI>
F;414-502/Domain: fibronectin type III repeat homology <PRI>
F;414-502/Domain: fibronectin type III repeat homology <PRI>
F;508-593/Domain: fibronectin type III repeat homology <PRI>
F;598-683/Domain: fibronectin type III repeat homology <PRI>
F;686-771/Domain: fibronectin type III repeat homology <PRI>
F;686-791/Domain: fibronectin type III repeat homology <PRI>
F;686-952/Domain: fibronectin type III repeat homology <PRI>
F;916-1045/Domain: fibronectin type III repeat homology <PRI>
F;9170-1172/Region: con Willebrand factor type A repeat homology <PRIP
F;1170-1172/Region: cell attachment (R-G-D) motif
F;1254-2793/Region: cell attachment (R-G-D) motif
F;253-2555/Region: cell attachment (R-G-D) motif
F;2784-2944/Domain: call attachment (R-G-D) motif
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R;Christiano, A.M.; Ryymaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly ---> Ser sul A;Reference number: A55255; MUID:94224777; PMID:8170945
A;Contents: annotation
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;17-2944/Product: collagen alpha 1(VII) che F;17-1253/Domain: amino-terminal nonhelical F;36-201/Domain: von Willebrand factor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: structural component of extracellular polymer C; Keywords: coiled coil; extracellular matrix; glycoprotein; F;1-16/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Map position: 3p21.3-3p21.3
A/Note: defects in this gene A/Note: there are 118 introns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hum. Mol. Genet. 2, 273-278, 1993
A;Title: The carboxyl-terminal half of type
A;Reference number: I48103; MUID:93271985; P
A;Accession: I84686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 815-892,'E',894-1439 <PAR>
A;Cross-references: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: 156328; MUID: 93107742;
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NyResidues: 'EPR',372-517,'DV',520-540,'W',542-1255 <RES>
NYResidues: 'EPR',372-517,'DV',520-540,'W',542-1255 <RES>
NYResidues: 'EPR',372-517,'DV',520-540,'W',542-1255 <RES>
NYResidues: 'EPR',372-5126,'NID:9262308; PIDN:AAB24637.1; PID:9262309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: GDB:COL7A1; EBR1; EBD1; EB
;Cross-references: GDB:128750; OMIM:120120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,Molecule type: mRNA, RE2>,Residues: 2395-2871,'S',2873-2944 RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Molecule type: protein ;Residues: 'A', 1240-1246, 'G', 1248-1250, 'XE', 1253-1255, 'Q', 1257, 'E'; 2032, 'C', 2034-2041; Note: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complex: type VII collagen is probably a homotrimer
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                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                              Query Match
Best Local
210
                                                                     154
                                                                                                     129
                                 187 SILKKSCI------EILAAEPST 203
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                                                                                                                                                                                                                                         17 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF---ISPQ-LRMSFIVFSTRGTT---LMKL
                                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                             Similarity
LVSRRVCTTAGGVPVTRPPDDSTSAPRDLVLSEPSS
                                                                                                   DLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIH 186
                                                                                                                                       GSGGDVIR-AIRELS--YKGGNTRTGAAILHVADHVFLPQLARPGVPKVCILITDGK-SQ 153
                                                                                                                                                                       TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHE 128
                                                                                                                                                                                                         DIVFLLDGSSSIGRSNFREVRSFLEGLVLPFSGAASAQGVRFATVQYSDDPRTEFGLDAL
                                                                   DLV---DTAAQRLKGQGVKLFAVGIKNADPEELKRVASQPTSDFFFFVND-FSILRTLLP
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                         7.3%;
                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                             Score 111.5;
Pred. No. 3.2
                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                         Gaps
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Search completed: June 13, 2005, 20:06:35 Job time: 21.0213 secs



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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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RA Altschenko L., Marusina K., Fermer A.A., Rubin G.M., Hong L.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA Richards S., McTeya K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Broch Marl B. Asa Schi II S.A Boalfaga-1500 full-length human
RT and mouse cDNA sequences.";
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"An unappreciated role for RNA surveillance.";
Genome Biol. 5:RESEARCH008.1-RESEARCH008.16 (2004).
-!- FUNCTION: Cellular role is not yet known.
-!- SUBUNIT: Binds to the protective antigen (PA) of Bacillus -!- SUBUNIT: Binds to the protective antigen (PA) of calcilus anthracis. Binding does not occur in the presence of calcilus -!- ALTERNATIVE PRODUCTS:
-!- ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100; Scobie H.M., Rainey G.J.A., Bradley K.A., Young J.A.T.; "Human capillary morphogenesis protein 2 functions as an anthra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH ANTHRAX TOXIN
                                                                                   but not in normal endothelial cells. DOMAIN: Binding to PA seems to be effected SIMILARITY: Belongs to the ATR family. SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                  TISSUE SPECIFICITY: Highly expressed in but not in normal endothelial cells.
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Eventealternative splicing; Named isoforms=6;

Comment=Experimental confirmation may be la
                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                            IsoId=Q9H6X2-1; Sequence=Displayed;
Note=May be produced at very low levels due to
codon in the mRNA, leading to nonsense-mediated
                                                                                                                                                                                                                                        IBOId=Q9H6X2-3;
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InterPro; IPR008399; Ant_C.
InterPro; IPR002035; VWF_A.
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H-InvDB; HIX0002125; -.
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PROSITE; PS50234; VWFA; 1
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AK025429; BAB15128.1;
AK001463; BAA91707.1;
BC012074; AAH12074.1;
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AF421380;
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          NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
                                                   LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL
                                                                                              LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQA
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NEKPFSVEDTYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
                                       LQGIIHSILKKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTL
                                                                                 LTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQA
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EDDD -> NKIK (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
Anthrax toxin receptor 1.
Extracellular (Potential).
                                                                                                                                                                                                                                                  /FTId=VSP 000448.
Missing (In isoform 4).
/FTId=VSP 000449.
B118A00AD5DF2233 CRC64;
                                                                                                                                                                                                                                                                                                                                               Missing (in isoform 2).
/FIId=VSP_000445.
NEKEPESVEDTYLLCPAPILKEVGMKAALOV
WVSSTSGFKEGNSHPCLPARPHT (in iso
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic 
VWFA.
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                                                                                                                                     LQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIA
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CC. - SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthrecis (By similarity).

CC. - Subcritilar I. From the protective antigen (PA) of Bacillus anthrecis (By similarity).
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MEDLINE=21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda
Kinzler K.W., St Croix B.;
                                This SWISS-PROT entry is copyright.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Antxr1; Synonyms=Atr,
Mus musculus (Mouse).
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                                                                                        SIMILARITY: Belongs to the ATR family. SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type I membrane ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative
                                                                                                                                                         IsoId-09CZ52-2; Sequence=VSP_000450; Note=No experimental confirmation available; MAIN: Binding to PA seems to be effected thr by similarity).
                                                                                                                                                                                                                                                                                                                  IsoId=Q9CZ52-1;
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   SWIBB
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Best Local
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InterPro; IPR008399; Ant C.
InterPro; IPR008399; VWF A.
Pfam; PF05587; Anth Ig; I.
Pfam; PF05586; Ant C; 1.
Pfam; PF00592; VWA; 1.
                                                                                                                                  LT 3
HUMAN
                                                    ATR2 HUMAN STANDARD; PRT; 489 AA. P58335; Q86UI1; Q8NB13; Q96NC7; 28-FEB-2003 (Rel. 41, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Anthrax toxin receptor 2 precursor (Capillary)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
DOMAIN
Name=ANTXR2; Synonyms=CMG2;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                       98.9%;
99.0%;
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N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
GRCINFTRVKMSQPAKYPLNNTYHPSSPPPAPIYTPPPPAPHCPPPASAPTPPIPSSPSTLPPPPQAPPNRAPPPSRPPPRPSV -> RFRGWRLTICLGSKHVHPGRHDKGPETPLLKQA
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 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                          protein-2)
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RA PLUMEGUSIA 10.2039; DUSTIO.1036/H94285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
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RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Cmura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi F., Yosida M., Hotuta T.,
RA Nomura Y., Tanai H., Kimata M., Watanabe S., Yosida M., Hotuta T.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Kusano J., Kanehori K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Nomiya S., Moniyama H., Satoh N., Takama S., Terashima Y., Suzuki O.,
RA Moriya S., Moniyama H., Satoh N., Takama S., Fujimori Y., Komaibe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA A Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matanira K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=14702039; DOI=10.1038/ng1285;
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Synovial cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 100:5170-5174(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100;
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MEDLINE=21539596; PubMed=11683410;
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                                                                                                                                                                                following preference: calcium > manganese > magnesium > zinc.
Seems to bind to collagen type IV and laminin.
SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).
Secreted (isoform 3). Isoform 1 is expressed at the cell surface while isoform 2 is predominantly expressed within the endoplasmic reticulum and not at the plasma membrane.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                 . Genet. 36:40-45(2004).
FUNCTION: Cellular role is not yet known.
SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis in a divalent cation-dependent manner, with the
                                                                                                                                                               Event=Alternative
                                                                   [BoId=P58335-2;
                                                                                                                 BoId=P58335-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ع
Sequence=VSP_008344, VSP_008345;
ental confirmation available;
                                                                 Sequence=VSP_008343;
                                                                                                               Sequence=Displayed;
                                                                                                                                                             splicing;
                                                                                                                                                               Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3),
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basement
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CARBOHYD
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                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:21732; ANTXR2
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                                                                                                                                                                                                                                                                                                                       VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative splicing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50234; VWFA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR008399; Ant C. InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P58335-4; Sequence=VSP_008346;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed in colon, heart,
liver, peripheral blood leukocytes, placenta, (
small intestine and spleen.
DOMAIN: Binding to PA seems to be effected thro
SIMILARITY: Belongs to the ATR family.
SIMILARITY: Contains 1 VMFA domain.
                                                                    155
                                              190
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PF00092; VWA; 1.
                                                                                                                97
                                                                                                                                     70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                   Similarity
                                                                              LFFYSEREANRSRDLGAIVYCVGVXDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
                                                                                                               GDRGKISKGLEDLKRVSPVGETYIHEGLKLANEQI--QKAGGLKTSSIIIALTDGKLDGL
                                                                                                                                  EDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHED
                                                                                                                                                                               PACYGGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLT
 TYLLCPAPILKEVGMKAALQVSMNDGLSFISSSVIITTTHCSDG
                      AQSCTEILELQPSSVCVGEEFQIVLSGRGFMLGSRNGSVLCTYTVNETYTTSVKPVSVQL
                                     KKSCIEILAAEPSTICAGESFQVVVRGNGFRHARNVDRVLCSFKINDSVTLNEKPFSVED
                                                                    VPSYAEKEAKISRSLGASVYCVGVLDFEQAQLERIADSKEQVFPVKGGFQALKGIINSIL
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489 AA;
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BAB70976.1; ALT_INIT.
BAC03731.1; -.
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53692
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                                                                                                                                                                                                                                                                                                                                                      WFA.

N-linked (GlcNAc...) (Potential).

N-linked (GlcNAc...) (Potential).

Missing (in isoform 2).

/FTIG=VSP_008343.

TLDVSVSFNGGKSVISGSLIVTATECSNGIAAI -> WGLT
TLDVSVSFNGGKSVITGGKSUTGSGSDPPTSAS (in isoform
                                                                                                                                                                                                                   Score 786;
Pred. No. 9.
                                                                                                                                                                                                                                                                ש
                                                                                                                                                                                                                                                                                                           Missing (In isofo /FTId=VSP_008345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
Anthrax toxin receptor 2.
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential). VWFA.
                                                                                                                                                                                                                                                                                                  VCIWECIEKELTA ->
                                                                                                                                                                                                                                                               /FTId=VSP_008346.
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                                                                                                                                                                                                                                                       B9F679DB75B6E2B7
                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                   008344.
                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                     6e-54;
                                                                                                                                                                                                                                                                                                                        isoform 3)
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centa, skeletal
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                                                                                                                                                                                                                             Length 489
                                                                                                                                                                                                                                                                BAC03731)
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AKEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;

AKIBAUSHER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

AKIBAUSHER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

AKIBAUSHER R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan K., Farmer A.A., Rabin G.M., Hong L.,

RA Hopkins R.F., Jordan K., Farmer A.A., Casavant T.L., Scheetz T.E.,

RA Hopkins R.F., Jordan K., Farmer A.A., Garcia A.M., Gay L.J., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RA Hithards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

VIllalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raha S.S., Loquellano B., Ketteman M., Madan A., Gay J.J., Hulyk S.W.,

VIllalon D.K., Muzny D.M., Sreen E.D., Dickson M.C.,

Raha S.S., Carlinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Pan J. Thea R. T. Marya M. A.
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR008309; Anth Ig.

InterPro; IPR008399; Ant_C.

InterPro; IPR008399; Ant_C.

Pfam; PP05807; Anth Ig; I.

Pfam; PP05806; Ant_C; I.

Pfam; PP059092; VMA; I.
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Eukaryota; Metazos; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00327; VWA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6; TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50234;
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            STRAIN-C57BL/6J; TISSUE=Testis;

MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.;

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Genome Res. 10:1757-1771(2000).
sequencing Genome Res. [6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome &
60,770 full-length cDNAs.";
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MEDLINE=99279253; PubMed=10349636;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933430J11 product:hypothetical Proline-rich regi
Willebrand factor type A domain containing protein, full insert
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Mammalia; Eutheria;
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A Adachi J., Alzawa K., Akimura T., Brakawa T., Bono H., Carninci P.,

A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

A Hori F., Imotani K., Jehii Y., Itoh M., Kagawa I., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Sano H.,

Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

B GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0016021; C:integral to membrane; IEA.

BR GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0016021; C:integral to membrane; IEA.

R Ffam; PF05587; Anth Ig; I.

P Ffam; PF05587; Anth Ig; I.
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Best Local
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Q96EC6;
01-DEC-2001
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
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STRAIN=C57BL/6J;
                                                                                                                                                         MEDLINE=22388257;
                                                                                                                                                                                                  TISSUE=Breast;
                                                                                                                                                                                                                                          SEQUENCE FROM
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Mammalia, Eutheria,
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTXR1 protein Name=ANTXR1;
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SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
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42.2%; Pred. No. 2.3e-39;
Live 58; Mismatches 105;
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Catarrhini; Hominidae; Homo
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annotation update)
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ıka T.,
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RESULT 7
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Best Local :
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR004400; Anth_Ig.
                                                                                                                                                                                                                                STRAIN-Sprague-Dawley;
O'Brien M.M., VanderVi
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Submitted
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SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DOWAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
                                                                                                FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of bloodborne pathogens, particulate matter, and senescent erythrocytes from the blood (By similarity)
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c. Natl. Acad. Sci. U.S.A.
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Soares M.B., Bonaldo M.F.,
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                                                                                                                                                                                                                                                                                                                                                                               precursor.
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Rodentia;
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Calcium; Cell adhesion; Glycoprot.
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Pfam; PF00357; Integrin_alpha;
Pfam; PF00092; VWA; 1.
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InterPro; IPR002035; VWF_A.
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DPQSLVDPIVQLQ----
                                                             DIAFLIDGSGSINORDFAOMKDFVKALMGEFASTSTLFSLMOYSNILKTHFTFTEFKNIL
                            DREQIRQGLEBLQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED
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Cytoplasmic (Potential).
FG-GAP 1.
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FG-GAP 4.
FG-GAP 5.
FG-GAP 6.
FG-GAP 7.
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RESULT 8
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INTERACTION WITH VCAM1.
INTERACTION WITH VCAM1.
MEDLINE=99059842; PubMed=9841932;
Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michael Gall
Hoffman P.A., Staunton D.E., Bochner B.S.;
"althadbeta2 integrin is expressed on human eosinophils and fi
"althadbeta2 integrin is expressed on the standard for vascular cell adhesion molecule"
                                                                                                                                                                                                                                                                                    Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R. Grayson M.H., Bochner B.S., Gallatin W.M., Staunton ("The leukocyte integrin alpha D beta 2 binds VCAM-1: binding interface between I domain and VCAM-1.";
                                                                                                                                                                                                                                                               binding interface between I doma J. Immunol. 163:1984-1990(1999).
                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH VCAM1.
MEDLINE=99370002; PubMed=10438935;
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Eukaryota; Metazoa;
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"Structural and functional characterization o
gene CD11d. Essential role of Sp1 and Sp3.",
J. Biol. Chem. 275:8959-8969(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96111956; PubMed-8777714; DOI-10.1016/1074-7613(95)90058-6; Van der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T., Staunton D.B., Gallatin W.M.; Staunton D.B., Gallatin W.M.; The Novel leukointegrin, alpha d beta 2, binds preferentially to ICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 171:291-294(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20187620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-235 FROM N.A.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exp. Med. 188:2187-2191(1998).
     FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICA VCAM1. May play a role in the atherosclerotic process sclearing lipoproteins from plaques and in phagocytosis borne pathogens, particulate matter, and senescent eryclerom the blood.

SUBUNIT: Heterodimer of an alpha and a beta subunit. All associates with beta-2.
SUBCELIULAR LOCATION: Type I membrane protein.

TISSUB SPECIFICITY: Expressed moderately on myelomonocy lines and subsets of peripheral blood leukocytes and st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2-integrin alpha subunit.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10722744; DOI=10.1074/jbc.275.12.8959;
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(Leukointegrin alpha
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Catarrhini; Hominidae
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EMBL; U37028; AAB38547.1; --
EMBL; U40274; AAB60634.1; --
EMBL; U40275; AAB60635.1; --
EMBL; U40276; AAB60637.1; --
EMBL; U40277; AAB60637.1; --
EMBL; U40279; AAB60637.1; --
EMBL; U40279; AAB60638.1; --
EMBL; U40278; AAB60638.1; JOINED.
EMBL; AF187881; AAF62875.1; --
HSSP; P11215; 1BHQ.
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MIM; 602453; -.
GO; GO:0008305; C:i
GO; GO:0016337; P:c
GO; GO:0007160; P:c
GO; GO:000955; P:c
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InterPro; IPR002035; WWF A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF009022; WWA; 1.
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PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5
SMART; SM00327; VWA; 1.
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                                                                                                                                                                                                                                                                                                                   PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
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atherosclerotic plaques, and on splenic red pulp macrophages.
DOMAIN: The integrin I-domain (insert) is a VWFA domain. Inte
with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain family.
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0008305; C:integrin complex; TAS. GO:0016337; P:cell-cell adhesion; NAS. GO:0007160; P:cell-matrix adhesion; NAS. GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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Cytoplasmic (Potential).
FG-GAP 1.
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Best Local S
Matches 67
                                                                                                       Miyazawa S., Azumi K., Nonaka M.;

"Cloning and characterization of integrin alph solitary ascidian, Halocynthia roretzi.";

J. Immunol. 166:1710-1715(2001).

-!- SUBCELLULAR LOCATION: Type I membrane prot.
-!- SIMILARITY: Belongs to the integrin alpha of the integrin alpha of the integrin alpha of the integrin alpha of the integrin alpha of the integrin alpha of the integrin alpha of the integrin alpha of the integrin alpha of the integrin alpha of the integrin alpha of the integrin integrin complex; IEA.

GO; GO:0005315; F:protein binding; IEA.
GO; GO:0007160; F:cell-matrix adhesion; IEA.
GO; GO:0007160; F:cell-matrix adhesion; IEA.
GO; GO:0007160; F:cell-matrix adhesion; IEA.
GO; GO:0007160; F:cell-matrix adhesion; IEA.
GO; GO:0007239; F:integrin-mediated signaling; Interpro; IPR002035; VWF_A.

Pfam; PF00902; VWA; 1.

Pfam; PF00902; VWA; 1.
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01-JUN-2001 (TrEMBLrel. 17, L
01-JUN-2003 (TrEMBLrel. 24, L
Integrin alpha Hrl precursor:
PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOMAIN
SMART; SM00191; Int alpha; 5
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
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NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=HrITGA1;
Halocynthia roretzi
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MEDLINE=21103187; PubMed=11160215;
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Missing (in Ref. 2).

GHPW -> ATP (in Ref. 2).

L -> V (in Ref. 2).

V -> A (in Ref. 2).
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Last sequence update)
Last annotation updat
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Pred. No. 0.
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                                                                                                                                                                                 pathway;
                                                                                                                                                                                                                                                                                                                                            chain
                                                                                                                                                                                                                                                                                                                                                                                                                                  subunits
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                                                                                                                                                                                                                                                                                                                                          (By similarity) in family.
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Query Match
Best Local S
Matches 65
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GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0005138; F:structural molecule activity; IE.

GO; GO:0007155; F:cell adhesion; IEA.

GO; GO:0007155; F:cell adhesion; IEA.

GO; GO:0006817; P:phosphate transport; IEA.

InterPro; IPR008161; Clighelix.

InterPro; IPR008160; Collagen.

InterPro; IPR008160; Collagen.

InterPro; IPR003129; TSP N.

InterPro; IPR003129; TSP N.

InterPro; IPR003035; VWP A.

Pfam; PF01391; Collagen; 16.

Pfam; PF01391; Collagen; 16.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8NFW1 PRELIMINARY; PRT; 1626 AA.
Q8NFW1;
Q8NFW1;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha 1 type XXII collagen.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell adhesion;
SIGNAL 1
CHAIN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Koch M., Jin W., Ashworth T. Submitted (AUG-2001) to the EMBL; AP406780; AAN03620.1; HSSP; P18614; 1MHP.
                                                                                                                                                                            PRINTS; PR00453; VWFADOMAIN.
ProDom; PD000007; Clg_helix;
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                    PROSITE; PS50234; VWFA; 1. Collagen.
SEQUENCE 1626 AA; 16111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEPSTICAGESFQVVVRGNGF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNKGIATFAVGVGEYDISELKLIASGTDSTDRVFTVTD-
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1332 AA;
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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A; 145851 MW; OD9108D2B05CFFAE CRC64;
                                                                                                    161115 MW;
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9.7%; Score 148.5; DB 2; 25.4%; Pred. No. 0.011; tive 45; Mismatches 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Burgeson R.E.;
EMBL/GenBank/DDBJ
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                                               Length
     Indels
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RESULT
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Best Local Similarity
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Q8T6U5;
Q9T6U5;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Proximal thread matrix protein 1 variant a.
Mytilus edulis (Blue mussel).
Mytilus edulis (Blue mussel).
Mytiloidea; Mytilidae; Mytilus.
Mytiloidea; Mytilidae; Mytilus.
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MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903;
Sun C., Lucas J.M., Waite J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matrix protein.
SEQUENCE 441
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SMART; SM00327; VWA; 2.
PROSITE; PS50234; VWFA; 2.
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EMBL; AF414454; AAL83537.1; -.
GO; GO:0005198; F:structural molecul
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                                                                                                                      TSSFNKLSKIMENVVKLACM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYGGFDLYFILDKSGSV----LHHWNEIYYFVEQLAHKF--ISPQ-LRMSFIVFSTRGTT 64
                                                                                                                                                                             NDGFQALQGIIHSILKKSCI 194
                                                                                                                                                                                                                                         VILLTDGQNNGHKS----PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-T 406
                                                                                                                                                                                                                                                                                                IIALTDGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPV 174
                                                                                                                                                                                                                                                                                                                                                                                                                LMKLTE--DREQIRQGLEELQKYLPG--GDTYMHEGFERASEQIYYENRQG---YRTASV 117
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Pred. No. 0.0025;
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                                                              SEQUENCE FROM N.A.

MEDLINE=88315033; PubMed=2457584;

Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;

Corbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.;

"The human leukocyte adhesion glycoprotein Mac-1 (compleme
type 3, CD11b) alpha subunit. Cloning, primary structure,
to the integrins, von Willebrand factor and factor B.";
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01-OCT-1996 (Rel.
25-OCT-2004 (Rel.
    SEQUENCE
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Name=ITGAM; Synonyms=CD11B,
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subunit) (CR-3 alpha chain) (CDl1b) (Leukocyte adhesion
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P11215;
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Sun C., Lucas J.M., Waite J.H.;
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SM00327; VWA; 2.
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PS50234; VWFA; 2.
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receptor |
J. Cell B
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MEDLINE=96363671; PubMed=8747460; DOI=10.1016/S0969-2126(01)00271-4;
Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway fo
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Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley "Cation binding to the integrin CD11b I domain and
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MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8; Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A., Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF
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                                                                                                                                               activation?";
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promoter of the CD11b gene directs
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Pierce M.W., Te
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Tenen D.G.;
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                     Mott J.E., V.H.;
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"Experimental support for a beta-propeller domain in integrin alpha-
subunits and a calcium binding site on its lower surface.";

Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).

-i- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
adhesive interactions of monocytes, macrophages and granulocytes
as well as in mediating the uptake of complement-coated particles.

It is identical with CR-3, the receptor for the iC3b fragment of
the third complement component. It probably recognizes the R-G-D
peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides
of fibrinogen gamma chain.

-I SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
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Structure 6:923-935(1998)
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DOMAIN: The integrin I-domain (insert)
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                                                                                                                                                                                                                              J03925; AAA59544.1;
J04145; AAA594903.1;
J52127; AAB24821.1;
S52152; AAB24821.1;
S52153; AAB24821.1;
S52154; AAB24821.1;
S52155; AAB24821.1;
S52156; AAB24821.1;
S52164; AAB24821.1;
S52167; AAB24821.1;
S52169; AAB24821.1;
S52169; AAB24821.1;
S52170; AAB24821.1;
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S52170; AAB24821.1;
S52170; AAB24821.1;
S52170; AAB24821.1;
S52170; AAB24821.1;
S52170; AAB24821.1;
S52180; AAB24821.1;
S52180; AAB24821.1;
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S52180; AAB24821.1;
S52180; AAB24821.1;
S52190; AAB24821.1;
S52190; AAB24821.1;
S52191; AAB24821.1;
S52212; AAB24821.1;
S52212; AAB24821.1;
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AAB24821.1;
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AAA58410.1;
AAA58610.1;
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Best Local (
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                                                                                                              QBT5C2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Proximal thread matrix protein 1.
Mytilus galloprovincialis (Mediterranean mussel).
Bukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorph.
byssal fibers.";
Biomacromolecules 3:1240-1248(2002)
EMBL; AY053391; AAL17974.1; -.
                                 MEDLINE=22313036; PubMed=12425661;
Sun C., Lucas J.M., Waite J.H.;
"Collagen-binding matrix proteins i
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SMART; SM00327; VWA; 1.
                                                                     SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=29158;
                                                                                                         Mytiloidea;
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SIGNAL
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PROSITE; PS50234; VWFA;
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Pfam; PF00357; Integrin_alpha;
Pfam; PF00092; VWA; 1.
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PRINTS; PRO0453; VWFADOMAIN.
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                                                                                                                                                                                                                                                        VNN-FEALKTIQNQLREK----IFAIEGTQTGSSSSFEHEMSQEGFSAA
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                                                                                                                                                                                                                                                                                                                               DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR----IADS--KDHVFP 173
                                                                                                                                                                                                                                                                                                                                                      FTFKEFQNNPNPRSLVKPITQLL-
                                                                                                                                                                                                                                                                                                                                                                             ----REQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALT 122
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@=143-334.
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                                                                                                                                                                                                                                                                                                                                                      - GRTHTATGIRKVVRELFNITNGARKNÁFKILVVIT
                                     from
                                                           DOI=10.1021/bm0255903;
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                                     elastomeric extraorganismic
                                                                                                                   Pteriomorphia;
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Best Local :
                                                                                                                                    Corbi A.L., Gardina Chem.
                                                                                                                                                                                                                (2)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-90153906; PubMed-2303426;
Corbi A.L., Garcia-Aguilar J., Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTAX HUMAN STANDARD; PRT; 1163 AA. P20702; QBIVA6; O1-FEB-1991 (Rel. 17, Created) O5-JUL-2004 (Rel. 44, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Integrin alpha-X precursor (Leukocyte adhesion alpha chain) (Leukocyte adhesion receptor p150,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            matrix protein.
SEQUENCE 453
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MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-88166645; PubMed=3327687;

COrbi A.L., Miller L.J., O'Connor K., Larson Corbi A.L., miller complete primary structure recond cloning and complete primary structure leukocyte adhesion glycoprotein, p150,95.";

EMBO J. 6:4023-4028(1987).
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=ITGAX; Synonyms=CD11C;
                                                                                                                                                                                                   Biol.
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m. 265:12750-12751(1990).
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25.5%;
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Pred. No. 0.0044
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subunit, the leukocyte p150,95
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,95) (CD11c) (Leu M5)
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e alpha subunit
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GO; GO:0008305; C:integrin complex; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0007155; F:cell adhesion; TAS.
GO; GO:0009887; P:organogenesis; TAS.
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00357; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gany L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickeon M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and p150,95 leukocyte adhesion proteins.";

J. Immunol. 138:2381-2383 (1987).

-I- FUNCTION: Integrin alpha-X/beta-2 is a receptor for fibrinogen. recognizes the sequence G-P-R in fibrinogen. It mediates cell-c interaction during inflammatory responses. It is especially important in monocyte adhesion and chemotaxis.

-I- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-X associates with beta-2.
                                                                                                                                                                                                                                                                                                                                                         EMBL;
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"Purification and alpha subunit N-terminal sequences and p150,95 leukocyte adhesion proteins.";
                                                                                                                                                                                                                                                 MIM;
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MEDLINE=87167596; PubMed=3549901;
                                                                                                                                                                                                                                                                   PDB; 1N3Y; X-ray;
Genew; HGNC:6152;
                                                                                                                                                                                                                                                                                  PIR; A36584;
PDB; 1N3Y; X-
                                                PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with I-domains do not undergo protease cleavage.
SIMILARITY: Belongs to the integrin alpha chain famil
SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains 1 VWFA domain.
DATABASE: NAME=PROW; NOTE=CD guide CDl1c entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdl1c.htm".
                                                                                                                                                                                                                                                                                                                  L; M81695; AAA59180.1; -.
L; M29165; -; NOT ANNOTATED CDS.
L; M29487; AAA51670.1; ALT SEQ.
L; M29482; AAA51620.1; JOINED.
L; M29483; AAA51620.1; JOINED.
L; M29484; AAA51620.1; JOINED.
L; M29485; AAA51620.1; JOINED.
L; M29486; AAA51620.1; JOINED.
L; M29486; AAA51620.1; JOINED.
L; M29486; AAA51620.1; JOINED.
L; M29486; AAA51620.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       granulocytes
DOMAIN: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: Predominantly expressed in
                                                                                                                                                                                                                                                   151510;
                    SM00327;
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 INTEGRIN ALPHA;
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Similarity 24.8%;
55; Conservative ;
                                       SLDYKD-VIPMADAAGIIRYAIGVGLAFONRNSWKELND----IASKPSOEHIFKVED-
                                                    LFFYSEREAURSRDLGAIVYCVGV------KDFNETQLARIAD--SKDHVFPVNDG
                                                                                                                                     DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE--
FDALKDIONQLKEK----IFAIEGTETTSSSSFELEMAQEGF
                  FQALQGIIHSILKKSCIBILAABPSTICAGESFQVVVRGNGF
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                   219
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Search completed: June 13, 2005, 20:03:14
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8: geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Example 4; SEQ ID NO 2121; 10078pp; English. Novel nucleic acids and polypeptides, useful as central nervous system injuries.

for treating

disorders

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WPI; 2001-442253/47. N-PSDB; AAI58132.

Tang YT, Liu C, Asundi V, (Wang J, Wang Z, Wehrman T, Zhou P, Goodrich R, Drmanac

Chen R, Xu C, IC RT;

Ma Xue Ą,ĸ

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Ren F, Zhang

Wang D; J, Zhao QA;

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
961	961	961	961	965	965	965	970	970	970	970	970	970	970	970	970	970	970	970	970
99.1	99.1	99.1	99.1	99.5	99.5	99.5	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Abu54438	Abu54492	Abb90785	Abb90731	Ad177138	Abg63873	Aae01469	Adr48216	Adm64578	Adj70017	Adi00552	Abu54431	Abu54457	Abp54904	Abb90724	Abb90750	Adm64576	Adi00550	Adm64592	Adm64590
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ALIGNMENTS

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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-UUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-CCT-2000; 2000US-00653036.
29-NOV-2000; 2000US-00727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; chemokinetic; thrombolytic; drug screening; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the CC encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system such as peripheral nervous injuries, peripheral neuropathy and coalised neuropathles and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic cativity, and Shy-Drager Syndrome. Other uses include the cutilisation of the activity such as: Immune system suppression, activiny. Another system suppression, and coalistic cand thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
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                                   Rottman
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                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                        fusion; von Willebrand factor A-like domain; vWF; antibacterial;
cutaneous; inhalation anthrax; human; TANGO 197 HisTag fusion; m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI00558 standard; protein; 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                    (HEAL/)
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                                                                  ROTTMAN J B.
O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
                                   JB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISFQLRMSFIVFSTRGTTLMKLTEDRE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297
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ilarity 100.0%;
Conservative 0
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                                   O'keefe
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                                    Ozkaynak
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Pred. No. 1.6e-99;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                       protein - plasmid p0615
                                   'n
                                    Healey JJ;
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                                                                                                                                                                                                                                                                                                                                                          fusion; mutant,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor Adomain (vWF) amino acid sequence and an amino acid sequence heterology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibacterial; gene therapy; von Willebrand factor A-like domain amino acid sequence; vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax; inhalation anthrax; human; TANGO197; his tag; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human TANGO197-His tag fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                               US2003134786-A1
                               Rottman
                                                                                                                                                                                                                            20-DEC-2001; 2001US-00038307
                                                                                                                                                                                                                                                                                20-DEC-2001; 2001US-00038307
                                                                                                                                                                                                                                                                                                                                           17-JUL-2003
                                                                                                                                        (ROTT/) ROTTMAN
(OKEE/) O'KEEFE
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                                                                                 ROTTMAN J B.
O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
                               'n,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; protein; 328
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                               O'keefe
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Pred. No. 1.8e-99;
; Mismatches 0;
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                               Healey JJ;
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Best Local :
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                                                                                                                                                                                                                             TANGO, 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis, psoriasis; inflammatory bowel disease; septic shock; ulcerative collitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease
                                                                                                                                                                           Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; sutoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis;
30-DEC-1998;
                                                               06-JUL-2000.
                                                                                                                                                                                                                                                                                                                Human TANGO
                                                                                                                                                                                                                                                                                                                                                  20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                               AAB01422 standard; protein; 333 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 328 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF.
                                23-DEC-1999;
                                                                                                                              Homo sapiens.
                                                                                                                                                               prophylatic,
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                                                                                                                                                               therapeutic;
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98US-00223546
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Pred. No. 1.8e-99;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyme's disease, cachexia and autoimmune diseases e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range of cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, remumatoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid sequences encoding TANGO-128, and 239 polypeptides useful for the treatment of arthritis, psoriasis and autoimmune diseases.
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N-PSDB; AAA47455.
                                                                                                                                                           Human anthrax toxin receptor.
                                                                                                                                                                                           08-JAN-2003
                                                                                                                                                                                                                        ABP54905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                              Protein
                                                                                                                               Anthrax; toxin;
                                                                                                                                                                                                                                                 ABP54905 standard; protein; 333
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                                                         Peptide
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                                                                                                                               receptor; human; antibacterial.
                              /label= Signal_peptide
28. .333
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Pred. No. 1.9e-99;
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asthma,
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ma, rheumatoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as a human anthrax toxin receptor (ATR) polypeptide on the basis of cidentity to a newly isolated human ATR (see ABP54903). The 2 polypeptides are identical between amino acids 1-317, but differ thereafter at the C-cerminus. The present polypeptide, encoded by IMAGE CLONE 4563020, has no previously known function, and there has been no prior indication that it is a complete or partial ATR. The invention provides ATR polypeptides and college polynucleotides, vectors, host cells, and transgenic and knock-out polynucleotides, vectors, host cells, and transgenic and knock-out animals. It also provides methods for identifying molecules that bind the CC ATR and which reduce the toxicity of anthrax toxin. A claimed method for treating anthrax in a human or animal involves administering an agent that inhibits binding between anthrax toxin protective antigen (PA) and ATR at a level effective to reduce the severity of anthrax. Suitable agents include the present polypeptide or a PA-binding fragment of it, a pa-binding polypeptide at least 80% identical to these, a fusion protein, a monoclonal or polyclonal antibody, a polysaccharide, a lipid or a
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      fusion;
                                                           Human TANGO 197 protein.
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      Willebrand factor A-like domain;
                                                                                                                          (first entry)
                                                                                                                                                                                                                                            protein;
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Best Local Similarity
Matches 187; Conserv
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antibacterial; gene therapy;
von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cu
                                                                  Human von Willebrand factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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(OKEE/)
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) O'KEEFE T L.
) OZKAYNAK E.
) HEALEY J J.
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                                                                                                                                                                                                                                                                                                                                                                                  QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
                                                                                                                                                            standard; protein;
                                                                                                                                                                                                                                                                                                                    SEREANRSRDIGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC 180
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                                                                                                                                                                                                                                                                                                      SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
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100.0%; Pred. No. 1.9e-99,
tive 0; Mismatches 0,
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                                                                  A-like domain protein TANGO197
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Matches 187;
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(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                           The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described ser: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a human von Willebrand factor A-like domain (vWF) amino acid sequence TANGO197.
            Human TANGO 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous
                                                   ADI00554;
                               22-APR-2004
                                                                      ADI00554 standard; protein;
                                                                                                                                                                                                                                                                                                                                         Sequence 333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 26; SEQ ID NO 2; 64pp; English.
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                              (first entry)
           FLAG fusion
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         protein -
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Pred. No. 1.9e-99;
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(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
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                                                                                                                                                                                                                                                                                     standard; protein; 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEILAAE 187
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Pred. No. 1.9e-99;
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Human TANGO197-FLAG

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Matches 187
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von Willebrand f
vWF amino acid s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ameliorating domain (vWF) to the vWF.
                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a fusion protein comprising human TANGO197 and FLAG that can be used to treat exposure to or prevent a symptom of anthrax.
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(OKEE/)
(OZKA/)
                ADI00556
                                          ADI00556
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O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
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                                                                                                                                                                                      SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSC 180
                                                                                                                                                                                                                              QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
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                                          standard;
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                                                                                                                                                                       SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
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rand factor A-like domain amino acid sequence;
acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
anthrax; human; TANGO197; FLAG; fusion protein; gene.
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                                         protein;
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                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                           Score 970; DB 7;
Pred. No. 1.9e-99;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                              The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWP. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 HiaTag fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                 New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (VWF) amino acid sequence and an amino acid sequence heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                           Sequence 345 AA;
                                                                                                                                                                                                                                                                                                                                                                Claim 45; SEQ ID NO 24; 86pp; English.
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                                                                                                                                                                                                         Local
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221
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O'KEEFE T L.
OZKAYNAK B.
HEALEY J J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI00555
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                                                                  SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
                                                                                                             QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
                                                                                                                                            GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE
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                                              SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
                                                                                              QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Willebrand factor A-like domain; vWF; antibacterial;
inhalation anthrax; human; TANGO 197 HisTag fusion; m
514; mutein.
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thrombin cleavage site
                       187
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Pred. No. 2e-99;
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                                                                                                                                                                                                                  DB 7;
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                                                                                                                                                                                                                   Length 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fusion; mutant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a fusion protein comprising human TANGO197, thrombin cleavage site and his tag that can be used to treat exposure to or prevent a symptom of anthrax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ameliorating symptoms of anthrax domain (vWF) amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 44; SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-2001; 2001US-00038307
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von Willebrand factor A-like domain amino acid sequence;
vWP amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; human; TANGO197; his tag; fusion protein; gene.
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DB; ADM64581.
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HEALEY J J.
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O'KEEFE T L.
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                                                                             SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSC 180
                                                                                                                                                     QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
                                            SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
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Pred. No. 2e-99;
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                                                   Novel isolated polypeptide useful for identifying reduces effect of anthrax toxin on host cell, for
                     Claim 1;
                                        human animal suffering from anthrax.
                                                                                    N-PSDB; ABV73881.
                                                                                                                                                              05-DEC-2000; 2000US-0251481P
                                                                                              WPI; 2002-713235/77.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human anthrax toxin receptor
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                                                                                                                    JAT,
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                                                                                                                                         WISCONSIN ALUMNI
                    Page 29-30;
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                                                                                                                  Bradley KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                              motif with amino acid
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motif with amino acid residues 50, 54, 118
                                                                                                                                                                                                                                                                                                                                                                                                                                 motif with
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motif with amino acid residues 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "PA-binding fragment, begins at any amino acid in the range 27-43 and ends at any amino acid in the range 221-321, region specifically described in Claim 3"
                                                                                                                                                                                                                                                                                                                              /note= "forms metal ion-dependent motif with amino acid residues 50,
                                                                                                                                                                                                                                                                                                                                                                /note= "forms metal ion-dependent
notif with amino acid residues 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227
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notif with amino acid residues 52, 54, 118
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                   45pp;
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present sequence is the protein sequence of a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial; gene therapy;
von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; human; TANGO197; immunoglobulin G; IgG;
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     N-PSDB;
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(OKEE/)
(OZKA/)
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Pred. No. 2.1e-99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a fusion protein comprising human TAMCO197 extracellular region, minus the DG residues closest to the transmembrane region, and immunoglobulin G (IGG) fragment of crystallisation (Fc) with mutations
                                                                                                                                                                                                                                                        foetal abnormality; developmental abnormality; haematopoietic di immune system disorder; AIDS; autoimmune disease; rheumatoid art inflammation; allergy; neurological disorder; Alzheimer's disease parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; condocrine disorder; infection; wound healing; vulnerary; cell cuchemotaxis; food additive; gene therapy; binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing cameliorating symptoms of anthrax comprises a von Willebrand factor domain (vWF) amino acid sequence and an amino acid sequence heterol to the vWF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 384 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-2001
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                                                                                                                                                                                                                                   chromosome 19
                              Protein
                                                                                    Peptide
                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; protein;
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                                                      /label= Signal_peptide
                                                                                                                   Location/Qualifiers
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Pred. No. 2.3e-99;
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                                                                                                                                                                                                                                                                                                  cell culture;
                                                                                                                                                                                                                                                                       identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The genes and their secreted proteins are useful for preventing, treating CC or ameliovating medical conditions, e.g., by protein or gene therapy.

CC Pathological conditions can be diagnosed by determining the amount of the conservative or the conditions can be diagnosed by determining the amount of the conservative discrete for the described for each of the 28 genes, conservative for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, conservative disorders, diseases of the immune system, AIDS, autoimmune considerative disorders (e.g., Alzheimer shin disease, Parkinson's disease), cognitive disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., cognitive disorders, schizophrenia, asthma, skin disorders (e.g., cognitive disorders, schizophrenia, asthma, skin disorders (e.g., cognitive disorders, schizophrenia, asthma, skin disorders, cognitive disorders, schizophrenia, asthma, skin disorders, cognitive disorders, kidney disorders, gastrointestinal disorders, cognitive disorders, kidney disorders, sand infections. The cognancy-related disorders, endocrine disorders, and infections. The corrections can also be used to aid wound healing and epithelial cell corrections, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding corrections and to chemotaxis, and can be used as food additive or proteins and can be used as food additive or proteins and can be used as food additive or proteins.
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1999; 99US-0163581P.
30-JUN-2000; 2000US-0215133P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein genes, and AAE01436-AAE01513 represent the AAE01514-AAE01544 represent human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD05300-AAD05379 represent cDNAs corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 485-486; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical condition used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                      187;
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                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                               QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
                                                                                                                                                                                                                                                          GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE 60
                                                                              SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC 180
                                                                                                                                        QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALIDGELHEDLFFY
                                                                                                                                                                                                                            GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE
                                                                                                                                                                                                                                                                                                                                                                                                            403
      IEILAAE 187
                                                  SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
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                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 2.4e-99;
0; Mismatches 0;
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tein fragments or variants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
                                                                                                                                                                                                                                          Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2000; 2000US-0229358P.
25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 874-875; 2102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New fusion protein for treating disease e.g. diabetes comprises albumin fused to a therapeutic protein.
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                    QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
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Search completed: June 13, 2005, 19:56:52 Job time : 71.2347 весв	221 IBILAAE 227	181 IBILAAE 187	161 SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSC 220	121 SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC 180

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Sequence 3, Appli	س -	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Patent No. 5424399	. 542	Sequence 43, Appl	Sequence 43, Appl	Sequence 5, Appli	Sequence 53, Appl	•	Sequence 53, Appl	-	53,			Sequence 53, Appl

ALIGNMENTS

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; SEQUENCE CHARACTERISTICS:
    LENGTH: 435 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: protein
PCT-US95-04439-1
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PCT-US95-04439-1
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GENERAL INFORMATION:
APPLICANT: The Up
APPLICANT: Heinri
                 Query Match
Best Local Similarity
   Matches
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TELEX: 224401
INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Gateway 2000 P5-90
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US95/04439
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Darrley, James D., Jr.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 476'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/385-5210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MAC-1 I-DOMAIN PROTEIN USEFUL IN TITLE OF INVENTION: BLOCKING ADHESION AND MIGRATION OF NEUTROPHILS NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 30
CITY: Kala
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kalamazoo
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301 Henrietta
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Heinrikson, Robert L.
Anderson, Donald C.
Tomich, Che-Shen C.
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 Conservative
14.7%; Score 142.5; DB 9 26.9%; Pred. No. 8.4e-08 tive 41; Mismatches 6
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V
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                                   Length
 Indels
                                     435;
 39;
Gaps
 11;
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-889-37
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US-08-286-889-37
; Sequence 37, A
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Best Local Similarity
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GENERAL INFORMATION:
                                                                                                                                        Matches
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FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/3216
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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APPLICANT: Van der
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
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ADDRESSEE: Marshall, O'Toole,
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                     TELEPAX: 25-3856
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                    142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
                                                                                                                                          53 ;
                                                                                                   4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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DPQSLVDPIVQLQ----
                               DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 116
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Van der Vieren, Monica
VENTION: No. 5470953el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                                                                                                                        312-474-0448
                                                                                                                                      14.6%;
ilarity 27.7%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                     37:
 --GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 256
                                                                                                                                          38;
                                                                                                                                      Score 141.5; DB 1;
Pred. No. 4.5e-07;
38; Mismatches 75;
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e, 6300 Sear Tower
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                                                                                                                                                                         Length 1151;
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                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Appresses: Marchall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
LENGTH: 1151 amino ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 278
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 23-DEC-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 23-DEC-1993
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                                                                                                                                          142
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117 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 LQGIIHSILKK 178
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                                                            DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 256
                                                                                                DREQIRQGLEELOKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 116
                                                                                                                                        DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
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                                                                                                                                                                                                                                                                                                                                                                          1151 amino acids
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                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27866/32797
                                                                                                                                                                                                                   Score 141.5; DB 1
Pred. No. 4.5e-07;
8; Mismatches 75
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; MOLECULE TYPE: protein
US-08-362-652-37
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                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino aci
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States ZIP: 60606-6402
   313
                                     168
                                                                                                                                          202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
                                                                                                                                                                                                                142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
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                                                                                                       LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 167
                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                     LQGIIHSILKK 178
                                                                     PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
LRSIQRQLQEK 323
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US-08-605-672-37
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Best Local Similarity
Matches 53; Conserv
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APPLICANT: Gallat
APPLICANT: Van de
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PRIOR APPLICATION DATA:
US 08/173,497
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
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TELEPHONE: 312-474-0448
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REFERENCE/DOCKET NUMBER: 27866/32684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LRSIQRQLQEK 323
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233 South Wacker Drive, 6300 Sear Tower
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                                                                             -GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
                                                                                                                                                       -GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
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RESULT 6
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RESULT 7
US-08-943-363-37
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Best Local :
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447
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CITY: Chicago
TTATE: Illinois
TTATE: Trnited
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APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
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PRIOR APPLICATION UMBER: US 08/173,497
PILLING DATE: 23-DEC-1993
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REFERENCE/DOCKET NUMBER: 278
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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                                                                     LRSIQRQLQEK 323
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233 South Wacker Drive, 6300 Sear Tower
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27.7%; Pred. No. 4.5e-07;
tive 38; Mismatches 75;
                                                                                                                                          -GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
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Best Local Similarity
Matches 53; Conserv
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION NUMBER: US 08/362,652
APPLICATION NUMBER: US 08/362,652
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APPLICANT: Gallatin,
APPLICANT: Van der V:
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SEQUENCE CHARACTERISTICS
LENGTH: 1151 amino ac:
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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313
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                                                                                                        117 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFFVNDGFQA 167
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LRSIQRQLQEK 323
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233 South Wacker
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27.7%; Pred. No. 4.5e-07;
ative 38; Mismatches 75
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5837478el Human
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RESULT 8 US-09-193-043-37

Sequence 37, Application US/09193043 Patent No. 6251395

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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 625195el Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/363,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
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ORGANISM: Rattue rattue

US-09-193-043-37
                                                                                                               PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR APPLICATION NUMBER: 08/605,672
PRIOR FILING DATE: 1996-02-22
PRIOR PILING DATE: 1993-12-23
PRIOR PILING DATE: 1993-12-23
PRIOR PILING DATE: 1994-08-05
PRIOR PILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR APPLICATION NUMBER: 08/362,652
PRIOR APPLICATION NUMBER: 08/943,363
PRIOR PILING DATE: 1994-12-21
PRIOR PILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6432404
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Mon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/09688307A
                                                                       SOFTWARE: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/688,307A CURRENT FILING DATE: 2000-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver.
                         LENGTH: 11
TYPE: PRT
ORGANISM: Rattus rattus
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                                                                                                PatentIn Ver. 2.0
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EARLIER APPLICATION NUMBER: 08/173,497
EARLIER FILING DATE: 1993-12-23
EEARLIER APPLICATION NUMBER: 08/286,889
EARLIER APPLICATION NUMBER: 08/266,889
EARLIER FILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 37
SENOTURE: 1151
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-350-259-37
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Patent No. 662091
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Best Local (
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OTHER INFORMATION: Xaa = NAME/KEY: misc_feature LOCATION: 1118
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6620915el Human 2
                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER FILING DATE: 1998-11-16
                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 27866/35004
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LOCATION: 464
OTHER INFORMATION: Xaa =
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OTHER INFORMATION: Xaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09350259
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27.7%; Pred. No. 4.5e-07;
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201 57

Query Match Best Local Similarity

14.6%;

Pred. No. 4.5e-07;

Length 1151;

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RESULT 11
US-08-485-618-55
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                      Matches
                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/362,652
FILING DATE: 21-DEC-1994
                                                                                                                                                                                         TELEVAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MERAL INFORMATION W. MICHAEL APPLICANT: Gallatin, W. MICHAEL APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5728533el
                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                      Local Similarity
                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                              NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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233 South Wacker Drive,
                                                                                                                                                                             1161 amino acids
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                    Conservative
                                                                                                                  protein
                  14.6%; Score 141.5; DB 1
27.7%; Pred. No. 4.5e-07;
tive 38; Mismatches 75
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e, 6300 Sear Tower
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                                                        DB 1;
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                      75;
                                                        Length 1161;
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US-08-362-652-55
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                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino aci
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 01
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 312-474-0448
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CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 LQGIIHSILKK 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 266
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                                          152 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL
    58 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 116
                                                                                                                    53;
                                                                              4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                                                                                                                                                                                                                                           1161 amino acids
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                                                                                                                      Conservative
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No. 5766850el Human 2 Integrin Alpha Subunit
                                                                                                                14.6%; Score 141.5; DB 1;
27.7%; Pred. No. 4.5e-07;
Mismatches 75;
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cker Drive, 6300 Sear Tower
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US-08-605-672-55
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; MOLECULE TYPE: protein
US-08-605-672-55
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                                                                                                                                         Query Match
Best Local Similarity 27.7
53; Conservative
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REFERENCE/DOCKET NUMBER: 271
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
ADDRESSEE: Marshall Macker Drive, 6300 Sear Tower
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 581751561 Human 2 Integrin Alpha Subunit
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APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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PRIOR APPLICATION UNDARA:
APPLICATION UNDABER: US 08/173,497
FILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 312-474-63
TELEPAX: 312-474-0448
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
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                                                                                                                                                                                                                                                                                                 amino acid
                                   DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 116
                                                                           DIAFLIDGSGSINORDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 211
                                                                                                              DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 266
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                                                                                                                                                        14.6%; Score 141.5; DB 2;
27.7%; Pred. No. 4.5e-07;
tive 38; Mismatches 75;
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                                                                                                                                                                                             Length 1161;
                                                                                                                                                        Indels
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US-08-482-293A-55
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GENERAL INFORMATION:
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PILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
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SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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STREET: Chicago
CITY: Chicago
Illinois
Thited
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                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 312-4.
                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 27866/32684
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117 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 LOGIIHSILKK 178
                                                                                                              152 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL
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                                                                       58 DREQIRQGLEBLQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGBLHED 116
                                                                                                                                                4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                                                                                                                                        Similarity
53; Conserv
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                                   DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
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                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                     14.6%; Score 141.5; DB 2
27.7%; Pred. No. 4.5e-07;
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cker Drive, 6300 Sear Tower
                                                                                                                                                                                      38;
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 Integrin Alpha Subunit
                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                       Length 1161;
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US-08-943-363-55
; Sequence 55, A
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                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1161 amino ac
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-363-55
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Patent No. 5837478
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., JOSEDH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: 312-474-630
TELEPAX: 312-474-0448
TELEX: 25-385
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                              Match 14.6%; Score 141.5; DB 2; Length 1161; Local Similarity 27.7%; Pred. No. 4.5e-07; les 53; Conservative 38; Mismatches 75; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                117 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 LRSIQRQLQEK 333
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                                                                                           212 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 266
                                                                                                                                                                                       152 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 211
                                                                                                                                       58 preqirqgleelqkvlpggdtymhegferaseqiyyenrqgyrta-sviialtpgelheb 116
                                                                                                                                                                                                                                  4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE-----
PLEYSDVIPAADKA---GIIRVAIGVGDAFQEPTALKELNTIGSAFPQDHVFKVGN-FAA
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233 South Wacker Drive, 6300 Sear Tower
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                                                                                                                                                                                                                                                                              Indels 25;
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Qy 168 LQGIIHSILKK 178
|: | : |
Db 323 LRSIQRQLQEK 333

Search completed: June 13, 2005, 20:05:09
Job time : 19.254 secs
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Maximum
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                                                                                                                                                                                                                                                                                                       and is derived
                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                            Score
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 June 13, 2005, 20:03:29 ; Search time 59.9593 Seconds (without alignments) 1195.537 Million cell updates/sec
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970
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Copyright (c) 1993 - 2005 Compugen Ltd
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     BG
US-10-038-307-26

US-10-201-292-26

US-08-796-753-12

US-10-038-307-2

US-10-201-292-2

US-10-201-292-22

US-10-201-292-22

US-10-201-292-24

US-10-201-292-24

US-10-201-292-24

US-10-201-292-28
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Sequence
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26, Appl
11, Appl
2, Appl
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22, Appl
22, Appl
22, Appl
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4.	550	550	550	550	550	900	949	949	949	949	949	949	949	949	960	961	961	961	961	965	970	970	970	970	970	970	970	970	970	970	970	970	970
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487	488	488	488	488	488	538	543	543	543	543	543	543	534	534	460	562	562	562	562	403	564	564	564	564	564	564	564	564	551	551	529	504	479
10	15	14	14	14	10	13	14	14	14	14	14	14	14			16						16				14				14		14	
-09-796-753-5	-10-104-047-	0-368-087-1	-10-201-292-	-10-038-307-	-09-796-753-5	-10-047-542-9	-10-201-292-1	-10-201-292-1	-10-201-292-	-10-038-307-	-10-038-307-1	07-1	-10-201-292-	-10-038-307-1	-10-201-292-	-10-474-7	-10-474-794-	-09-918-715-30	-09-918-715-1	-09-833-245-62	0-474-794-	-10-474-794-18	-10-408-765A-1	-10-301-822-	-10-201-29	0-038-307-	-09-918-715-23	-09-918-715-18	-10-201-292-1	-10-038-30	-10-201-292-3	-10-201-292-3	9
10	26	Sequence 16, Appl	9	è.	52	99	16,	14,	10,	16,	14,	10,	12,	12,	e 30,	e 301,	e 194,	e 301,	194	620,	e 232	187	182	199	e 20,	20,	equence 232	e 187	e 18,	e 18,	e 36,	e 34,	Sequence 32, Appl

ALIGNMENTS

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S
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SOPTWARE: PRECSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 328
TYPE: PRT
CORGANIZM: Homo sapiens
US-10-038-307-26
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                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 187; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/10038307
Publication No. US20030134786A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEPE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-599
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILLING DATE: 2002-06-28
                                     101
121 SERBANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC 180
                                                                                                                41
                                                                         61 QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY 120
                                                                                                            QIRQGLEBLQKVLPGGDTYMHEGPERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY 160
                                                                                                                                                                                    100.0%; Score 970; DB 14;
100.0%; Pred. No. 6e-93;
                                                                                                                                                                                                                             DB 14; Length 328;
                                                                                                                                                                                        Indels
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                                                                                                                                                                                        Gaps
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CURRENT APILICATION NUMBER: US/10/201,292
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 26
; SEQ ID NO 26
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-26
           APPLICATION CONCERTS
APPLICATION: MCCARTEN, Sean A.
FILE REFERENCE: 7853-227-999
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR PILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR FILING DATE: 1999-03-03
PRIOR FILING DATE: 1999-03-03
PRIOR FILING DATE: 1999-03-03
PRIOR FILING DATE: 1999-03-03
PRIOR FILING DATE: 1999-03-03
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US-09-796-753-12
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US-10-201-292-26
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                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09796753 Publication No. US20030027998A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 970; DB 14; Length 328; Best Local Similarity 100.0%; Pred. No. 6e-93; Matches 187; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNA
APPLICANT: Engin OZKAYNA
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEILAAE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEREANRSRDIGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSC 180
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No. US20030144193A1
   NUMBER:
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PRIOR PILING DATE: 2000-09-
PRIOR APPLICATION NUMBER: (
PRIOR FILING DATE: 2000-09-
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 12
LENGTH: 333
                                                                      RESULT 4
US-10-038-307-2
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Sequence 2, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 187; Conservative
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APPLICATION NUMBER: 09/474,072
FILING DATE: 1999-12-29
APPLICATION NUMBER: 09/514,010
FILING DATE: 2000-02-25
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FILING DATE: 1999-12-23
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Gaps

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APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEPE

APPLICANT: Engin OXAYYAK

APPLICANT: Judith J. HEALEY

ITITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REPERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PASTSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 333

TYPE: PRT

ORGANISM: Homo Sapiens
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-2
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Best Local Similarity
Matches 187; Conserva
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Matches 187; Conserv
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SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 2
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CURRENT FILING DATE: 2002-06-28
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   161
                         121 SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSC
                                                                           101 QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
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SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
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Judith J. HEALEY
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                                                                                                                                                                                                                                            100.0%; Score 970; DB 14; Length 333; 100.0%; Pred. No. 6.2e-93;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-22
                                                                                          ) ORGANISM: Homo sapiens US-10-201-292-22
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US-10-038-307-22
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                                                                                                                                                  APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-99
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
THE TENGTH: 342
  Best Loca
Matches
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOPTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
TENCETH: 342
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                                              Query Match
                                                                                                                                      TYPE: PRT
  Local Similarity
les 187; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/10201292
100.0%; Score 970; DB 14; ilarity 100.0%; Pred. No. 6.4e-93; Conservative 0; Mismatches 0;
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                                              DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14;
                                            Length 342;
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220 180 160 120 100 60 0

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Sequence 24, Application US/10201292

Publication No. US:0030144193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FASTSEQ for Windows Version 4.0
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US-10-038-307-24
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US-10-038-307-24
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LENGTH: 345
TYPE: PRT
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APPLICANT: James B. ROTTWAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Sudith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-99

CURRENT FILING NOUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR RETLING DATE: 2000-02-6, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR PILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 621
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-621
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Publication No. US20
GENERAL INFORMATION:
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LENGTH: 345
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local 8
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TITLE OF INVENTION: Albumin Fusion Proteins
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                                                                  IBILAAE
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; ORGANISM: Homo sapiens
US-10-201-292-32
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; ORGANISM: Homo sapiens
US-10-201-292-28
                                                                                                                                                                                                                                                                                                                                       APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Dudith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 32, Application US/10201292 Publication No. US20030144193A1 GENERAL INFORMATION:
                                                                                                                                                                      Query Match 100.0%; Score 970; DB 1
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 187; Conservative 0; Mismatches
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Bogin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REPERENCE: 7853-959 197 and Tango 216 Compositions and Methods
FILE REPERENCE: 7853-959 197 and Tango 216 Compositions and Methods
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                            LENGTH: 479
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                        QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY 120
                                                                                                                GGFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE
QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
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                                                                                                                                                                                                              DB 14; Length 479;
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APPLICANT: James B. ROTTMAN
APPLICANT: Therees L. O'KERFE
APPLICANT: Therees L. O'KERFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
PILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 504
TYPE: PAT
ORGANISM: Homo sapiens
US-10-201-292-34
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US-10-201-292-36
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US-10-201-292-34
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; ORGANISM: Homo sapiens
US-10-201-292-36
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                                      SOPTWARE: FastSEQ for
SEQ ID NO 36
LENGTH: 529
TYPE: PRT
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Publication No. US20030144193A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Login OZKAYNAK
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
                                                                                                                   NUMBER OF SEQ ID NOS:
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                                                                                                    Windows Version 4.0
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Pred. No. 1.1e-92;
Mismatches 0;
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Sequence 18, Application US/10038307

Publication No. US20030134786A1

GENERAL INFORMATION:
APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: JUGALTH J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION STATE
SOFTWARE: FRASTSEQ for Windows Version 4.0

SEQ ID NO 18
LENGTH: 551
Search completed: June 13, 2005, 20:36:50 Job time : 59.9593 secs
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US-10-038-307-18
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Maximum Match 100%
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     Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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A4WU1B
A40020
A45638
RWHU1C
S00551
C2MS
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T23087
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T46488
A37979
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I51027
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8 8 8 8 8	Query Best Match	MO1. Bi A;Refer A;Refer A;Statu A;Mo1ed A;Mo1ed A;Resid A;Cross A;Note	RESULT 1 A48569 Antigen C;Specic C;Date: C;Dace: C;Dace: R:Pasama	
107 QNAD 117 LFFY 162 165 FQAL 218 WGGV	Match socal Sage 53	Mol. Biochem. Parasitol. 57, 171-174, A;Title: Sequence of a major Eimeria r A;Heference number: A48569; MUID:9314; A;Accession: A48569 preliminary A; Molecule type: nucleic acid A;Residues: 1-724 <pas> A;Coss-references: UNIPROT:004588; Gi A;Cross-references: UNIPROT:004588; Gi A;Cross-ref</pas>	RESULT 1 A48569 antigen Em100 - Bimeria m C;Species: Bimeria maxima C;Date: 01-Dec-1993 #sequ C;Accesion: A48569 R:Pasamontes. L.: Hug. D.	93 88 99 87 88 99 87 88 99 87 98 87 98 98 87 98 97 97 98 97 98 97 98 97 98 97 98 97 98 97 98 97 98 97 98 97 98 97 97 98 97 97 98 97 98 97 98 97 98 97 98 97 98 97 98 97 98 97 98 97 98 97 97 98 97 97 98 97 98 97 98 97 98 97 98 97 98 97 98 97 98 97 98 97 98 97 9
QIRGELIGAVLPY QNADLLAAAAKKLPY QNADLLAAAAKKLPY LFFYSEREA SSRRSQTLSAA FQALQGIIHSILKKS : :	14. Similarity 26. 3; Conservative DLYFILDKSGSV-LH :: : : DVMLVVDESGSIGTS	usitol. of a musical mary is A485is cylor cylor cylor ixtract: cylor ixtract: cylor cylor ixtract cylor cylo	Bimeria maxima ia maxima 93 #sequence_ 569 Hug. D.: Hum	88888888999999999999999999999999999999
QIKGUBBUQKUFT-GGU QNADLLAAAAKKLPYAAGS' LFFYSEREANRSR SSRRSQTLSAAEKLR FQALQGIIHSILKKSCIEI 	14.1%; 26.6%; ative SV-LHHWN : :: SIGTSNYG	ajor Ein 59; MUI 69; MUI acid acid ed from lebrandi spondi spondi spondi spondi spondi	maxima a uence_revisi	341 2 341 2 341 2 341 2 141 2 141 2 141 2 141 2 141 2 141 2 141 2 141 2 141 2 141 2 141 2 141 2 141 2 141 2 141 3 141
	Score 137; DB 2; Le Pred. No. 0.0007; 38; Mismatches 80; SIYFVEQLAHKF-ISP-QLRMS ::	1993 naxima antigen package siM99058; NID:8 packbone (NCBIN c type A repeat homol l repeat homol l repeat homol l repeat homol l repeat homol l repeat homol l repeat homol l repeat homol	LIGNMENTS . 18-Nov-1994	A40970 E70121 A37797 JC5953 T30889 T32949 AG2350 AG2285 B83262 H90261 T05901 F84811 AB1079 ITECAP B91018 D85862
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RESULT 2
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Call surface glycoprotein CD11b precursor [validated] - human

cell surface glycoprotein CD11b precursor [validated] - human

cell surface glycoprotein CD11b precursor [validated] - human

cell surface glycoprotein CD11b precursor [validated] - human

considerate names: complement receptor type 3 alpha chain; leukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain

considerate: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

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considerate names: complement receptor type 3 alpha chain; leukocyte adhesion

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considerate names: complement receptor type 3 alpha chain;

protein

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R;Hicktein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J. Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: CDNA sequence for the alpham subunit of the human neutrophil adherence receptions. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: CDNA sequence for the alpham subunit of the human neutrophil adherence reception: A32218
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A;Title: Structural analysis of the CD11b gene and phylogenetic analysis of the alpha n during evolution.
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A;Note: the last three bases of intron 13, CAG, are included in some but not all matural process of the sequence extracted from NCBI backbone (NCBIP:121963)
A;Peterce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
Biochim. Biophys. Acta 874, 368-371, 1986
A;Title: N-terminal sequence of human leukocyte glycoprotein Mol: conservation across A;Accession: A26091
A;Accession: A26091
A;Accession: A26091
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A; Mote: part of this sequence was confirmed by protein sequencing
R; Arnaout, M.A.; Gupta, S.K.; Pierce, M.W.; Tenen, D.G.
J. Cell Biol. 106, 2153-2158, 1988
A; Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion receptor M
A; Reference number: A28915; MUID:88257215; PMID:2454931
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R;pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
A;Title: Characterization of the myeloid-specific CD11b
A;Reference number: I52567; MUID:92144986; PMID:1346576
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                                             A;Accession: I52567
A;Status: translated
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                                                   from
                                                   GB/EMBL/DDBJ
                                                                                                                                                                                                             promoter.
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A;Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:g22281
A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and R;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and R;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and R;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and A;Note: in the authors' translation residues 1216-1219 are shown after residues 1235 and A;Note: in the authors' translation residues 1216-1219 are shown after residues 1235 and A;Note: in the authors' translation residues 1216-1219 are shown after residues 1235 and A;Note: in the authors' translation residues 1236-1219 are shown after residues 1235 and A;Note: in the authors' translation residues 1236-1219 are shown after residues 1235 and A;Note: in the authors' translation residues 1236-1219 are shown after residues 1236-1219 are shown after residues 1236-1219 are shown after residues 1236-1219 are shown after residues 1236-1219 are shown after residues 1236-1219 are shown after residues 1236-1219 are shown after residues 1236-1219 are shown after re
R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by
                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL;J05137; NID (211284; PIDN:AAA48635.1; PID:g211285
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A;Introns: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1 C;Keyword8: alternative splicing; cell binding; coiled coil; connective tissue F;1-23/Domain: signal sequence #status predicted <SIG>F;2-3124/Product: collagen alpha 1(XII) chain #status predicted <MAT>F;24-114/Domain: IIIA #status predicted <IIIA>F;24-114/Domain: IIIA #status predicted <IIIA>F;24-114/Domain: collagen alpha 1(XII) chain short splice form #status F;24-114/Domain: IIIA #status predicted <IIIIA>F;24-114/Domain: von willebrand factor type A repeat homology <FW3A>F;33-414/Domain: fibronectin type III repeat homology <FW3B>F;332-414/Domain: fibronectin type III repeat homology <FW3C>F;629-1178/Domain: fibronectin type III repeat homology <FW3C>F;629-1178/Domain: fibronectin type III repeat homology <FW3B>F;610-911/Domain: fibronectin type III repeat homology <FW3B>F;995-1076/Domain: fibronectin type III repeat homology <FW3G>F;1086-1169/Domain: fibronectin type III repeat homol
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F;2438-2440/Region: cell adhesion #status predicted
F;2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status
F;2751-2902/Domain: collagenous COL2 #status predicted <COL2>
F;2899-2901/Region: cell attachment (R-G-D) motif
F;2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>
F;2946-3048/Domain: collagenous COL1 #status predicted <COL1>
F;3946-3048/Domain: non-collagenous NC1 #status predicted <NC1>
F;3049-3114/Domain: non-collagenous NC1 #status predicted <NC1>
F;3049-3124/Domain: non-collagenous NC2 #status predicted <NC1>
F;3049-3124/Domain: non-collagenous NC2 #status predicted <NC2>
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A; Residues: 2831-2832,'T', 2834,'R', 2836-2843;3002-3014 <D
R; Trueb, B:
Biochim. Biophys. Acta 1171, 97-98, 1992
A; Title: The two splice variants of collagen XII share a
A; Reference number: $28811; MUID:93042014; PMID:1420368
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A,Residues: 1-24,1189-1257,'8',1259-1263,'E',1265-1280 <TRU>
A,Cross-references: EMBL:X67327
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J. Blol. Chem. 262, 17724-17727, 1987
A;Title: Type XII collagen is expressed in embryonic chick tendons.
A;Reference number: S22254; MUID:88087065; PMID:3121603
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A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517
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A; Residues: 2960-2976, 'F', 2978-3074, 'AG' <GOR3>
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F;1474-1557/Domain:
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A;Accession: A28037
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      Query Match
Best Local Similarity
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in: fibronectin type 
             13.3%;
28.2%;
             Score 129;
Pred. No.
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                   0.02;
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H
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992
C;Accession: A36584; A35543; S00864
R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 12750-12751, 1990
                                                                                                                                                                                                                                                                                                                            cell surface glycoprotein CD11c precursor - hum N; Alternate names: leukocyte adhesion receptor
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F;238-296/Domain: thrombospondin type 1 repeat homology <THRÎ>F;309-371/Domain: thrombospondin type 1 repeat homology <THR2>F;309-371/Domain: thrombospondin type 1 repeat homology <THR3>F;372-432/Domain: thrombospondin type 1 repeat homology <THR4>F;433-493/Domain: thrombospondin type 1 repeat homology <THR4>F;494-556/Domain: thrombospondin type 1 repeat homology <THR5>F;560-610/Domain: thrombospondin type 1 repeat homology <THR6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:043981; GB:AF032905; GB:M73495; NID:g2707732; PIDN:AAD03350.
A;Note: sequence extracted from NCBI backbone (NCBIN:77752, NCBIP:77756)
F;48-218/Domain: von Willebrand factor type A repeat homology <VWA1>
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A45638
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A; Residues: 1-712 < TOM>
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C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Title: Sequence of the gene encoding an immunodominant microneme;Reference number: A45638; MUID:92131064; PMID:1775171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
ol. Biochem. Parasitol. 49, 277-288, 1991
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  216 SNWSNVTQQVNGIIKAACKDL
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                                                                                        LVMTDGA--SNLPSQTRSSÄAALRDAGÄTVVVLGVGSGVNSSECRSTÄGCSTSNCPRYLQ
                                                                                                                                  IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFP--VN 162
                                                                                                                                                                              KVRWNLSDPKATNPSLAISAARSLSYSTGVTYTHYGLQDA-KKLLYDTNAGARNNVPKLV 157
                                                                                                                                                                                                                          QIRQGLEELQKVLPG-
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                                              DGFQALQGIIHSILKKSCIBI
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                                                                                                                                                                                                                                                                                                                                                          Score 128.5; Db 2;
Pred. No. 0.0037;
Pred. No. 0.0037;
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human

p150,95 alpha chain

#text_change 09-Jul-2004

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leukocyte surface glycoprotein Mac-1 alpha chain precursor - N;Alternate names: complement-3 receptor alpha chain C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence revision 30-Sep-1991 #text_charC;Accession: S00551; IS9078
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A;Map position: 16pl1.2-16pl1.2
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat home c;Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat; Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repeat; F;1-19/Domain: signal sequence #status predicted <SIG>F;20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>F;20-1107/Domain: extracellular #status predicted <EXT>F;149-319/Domain: von Willebrand factor type A repeat homology <VWA4>F;1134-1163/Domain: transmembrane #status predicted <INM>F;1134-1163/Domain: transmembrane #status predicted <INM>F;1134-1164/Dimain: #status predicted <INM>F;1134-1164/Dimain: transmembrane #status 
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A;Residues: 1-755, 'L', 757-1163 <CO3>
A;Residues: 1-755, 'L', 757-1163 <CO3>
A;Residues: 1-755, 'L', 757-1163 <CO3>
A;Crose-references: GB.M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
C;Genetics:
C;Genetics:
A;Gene: GDB:ITGAX; CD11C
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A;Title: cDNA cloning and complete primary A;Reference number: S00864; MUID:88166645;
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A;Title: Genomic structure of an integrin alpha subunit, the leukocyte pl A;Reference number: A35543; MUID:90153906; PMID:2303426
A;Accession: A35543
A; Accession: S00551
A; Molecule type: DN
                                                                                  A; Title: Amino acid sequence of the murine A; Reference number: S00551; MUID:88312584;
                                                                                                                                                                         R;Pytela, R.
EMBO J. 7, 1
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A; Residues: 1-834 < CO2>
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A;Cross-references: UNIPROT:P20702
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A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 NPLSLLASVHOLO-----GFTYTATAIONVVHRLFHASYGARRDATKILIVITDGKKEGD
                                                                                                                                                                              1371-1378,
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K.; Larson, R.S.; S
                                                                                  Mac-1 alpha chain
PMID:3044779
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A;Cross-references: UNIPROT:P21180; GB:M57891; GB:J05661; NID:g192436; PIDN:AAA63294.1; R;Ishikawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, H.R. J. Biol. Chem. 265, 19040-19046, 1990
J. Biol. Chem. 265, 19040-19046, 1990
A;Title: Murine complement C2 and factor B genomic and cDNA cloning reveals different m A;Reference number: A36593; MUID:91035430; PMID:2229060
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A;Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983
A;Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983
A;Note: the authors translated the codon CAC for residue 569 as Gln
R;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts,
Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A;Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept
A;Reference number: 159078; MUID:86287312; PMID:2942940
                                                                                                                                               A;Cross-references: EMBL:M57891; NID:g192436; PIDN:AAA63294.1; PID:g192437 R;Falus, A.; Wakeland, E.K.; McConnell, T.J.; Gitlin, J.; Whitehead, A.S.; Immunogenetics 25, 290-298, 1987 Immunogenetics 25, 290-298, 1987 A;Title: DNA polymorphism of MHC III genes in inbred and wild mouse strain: A;Reference number: I54429; MUID:87192938; PMID:2883115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Ishikawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, submitted to GenBank, January 1991 A;Reference number: A38875
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C;Superfamily: cell surface glycoprotein CD11b; von Willebrand
C;Keywords: cell adhesion; glycoprotein; transmembrane protein
A;Residues: 660-677, 'R',679,681-723, 'G',725
A;Cross-references: GB:M16271; NID:g199289;
                                                                               A;Accession: 154429
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-760 <ISH>
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A; Residues: 1-760 < IS2 >
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C; Accession: A38876; B36593; T54429
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A;Cross-references: GB:M14293; NID:g198993; PIDN:AAA39484.1; PID:g554193
                                                               A; Molecule type: mRNA
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Pred. No. 0.0
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   <RES>
PIDN:AAA39562.1;
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      PID:g199290
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C;Genetics: 16/1.
A;Introns: 16/1.
C;Complex: The I
C;Function:
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A;Reference number: $42368
A;Accession: $42373
A;Molecule type: DNA
A;Refidues: 1-3051 <SMI>
A;Cross-references: EMBL:Z30423; NID:g458479; PID:g458485
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1-18/Domain: signal sequence #status predicted <SIGs
F;19-250/Product: complement C2b fragment #status predicted <C2B>
F;22-89/Domain: complement factor H repeat homology <FH1>
F;94-149/Domain: complement factor H repeat homology <FH2>
F;156-210/Domain: complement factor H repeat homology <FH2>
F;151-760/Product: complement C2a fragment Brown #status predicted <C2A>
F;251-760/Product: complement C2a fragment long form #status predicted <C2A>
F;251-605,613-760/Product: complement C2a fragment Bhort form #status predicted <C2S>
F;251-49/Domain: von Willebrand factor type A repeat homology <VFA>
F;250-449/Domain: trypsin homology #status atypical <TRY>
F;262-62,49-89,94-136,122-149,156-197,182-210,470-590,499-515,593-609,647-674,685-715/Dis
F;271,117,297,340,474,478,663/Binding site: Carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T20G5.3 - Caenorhabditis elegans C/Specides: Caenorhabditis elegans Croate: 07-Oct-1994 #sequence_revision 10-Nov-1995 #t/C/Accession: S42373
R/Smith, A.
                                                                                                                                                                                                                                                                                                                                                                                                  A;Introne: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1 F;512-679/Domain: von Willebrand factor type A repeat homology <VWA1> F;754-793/Domain: fibronectin type II repeat homology <2F1>
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A,Pathway: complement classical pathway
C,Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology;
C,Keywords: alternative splicing; complement classical pathway; duplication; glycoprote
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                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 55
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                                                                                                                       514 DLVPLIDGSGSIGSYVFKNEVLRFVREFVELFEIGRSKTRVGLIQYSDQIRHEFDLDQYG 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 LNE--LGSKKDGERHAFILQDA-KALQQIFEHMLDVS 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 FNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 KEIRHTIILLTDGK--SNMGDSPKKAVTRIRELLSIEQNRDDYLDIYAIGVGKLDVDWKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 ----VIIALTDGELHEDLFFYSEREANRSRDLGAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 ERSQ-----DVTEVITSLDSASYKDHENATGANTYEVLIRVYSMMQTQMDRLGMETSAW 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16/1; 91/1; 153/1; 212/1; 245/3; 290/3; 337/1; 384/1; 414/1; 461/1; 492/3; 53 The proenzyme forms a complex with C4a and is activated by cleavage into C2a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE-----NRQGYRTAS- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                4 DLYFILDKSGSVLHH--WNEIYYFVEQLAHKFI--SPQLRMSFIVFSTRGTTLMKLTE-- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGFDLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTE 57
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
DRDSLLKGISETQ-YLTGLTRTGAAIQHMVQEGF-----SERRGARPQQSDIARVA
                                                         DREQIRQGLEELQKVLPG----GDTYMH---EGFERASEQIYYENRQGYR-----TASVI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHLNLYLLLDASQSVTEKDFDIFKKSABLMVERIFSFEVNVTVAIITFASQPKTIMSILS
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                                                                                                                                                                                                                                                                           12.0%; Score 116; DB 28.2%; Pred. No. 0.25;
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                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #text_change 09-May-2004
                                                                                                                                                                                                                                                                                                        Length 3051;
                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                 34;
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F:40-204/Domain: von Willebrand factor type A repeat homology < PN3A- F:236-409/Domain: fibronectin type III repeat homology < PN3A- F:326-409/Domain: fibronectin type III repeat homology < PN3B- F:418-498/Domain: fibronectin type III repeat homology < PN3C- F:507-591/Domain: fibronectin type III repeat homology < PN3D- F:507-591/Domain: fibronectin type III repeat homology < PN3B- F:507-7/Domain: fibronectin type III repeat homology < PN3F- F:716-798/Domain: fibronectin type III repeat homology < PN3F- F:716-798/Domain: fibronectin type III repeat homology < PN3F- F:806-893/Domain: von Willebrand factor type A repeat homology F:91111-1352/Domain: non-collagenous NC2 #status predicted < NC2- F:1511-1553/Domain: non-collagenous NC2 #status predicted < NC3- F:1511-1553/Domain: non-collagenous NC2 #status predicted < NC3- F:1511-1553/Domain: non-collagenous NC2 #stat
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A; Residues: 1551-1570; 1593-1599; 1639-1667 < GOR2 > C; Keywords: alternative splicing; coiled coil; es
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne, Eur. J. Blochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens A;Reference number: S17035; MUID:92037585; PMID:1935930
A;Accession: S17035
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Eur. J. Biochem.
A;Title: Type XI'
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C;Accession: A45974; S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Duble
J. Biol. Chem. 268, 12177-12184, 1993
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A;Experimental source: embryo skin
A;Note: sequence inconsistent with the nucleotide translation
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C;Species: Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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A; Residues: 1472-1659 < GORl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1472-1660 < APT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collagen alpha 1(XIV) chain precursor, short form 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: S20833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary
                                               Best
                                                                                Query Match
                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.; Trueb, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU>
K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IILTDGRSQDNV----TGPADSARKLSINTFAIGVTDHVLASELESIAGSPNRWFYV-DK 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGVKD-FNETQLARIADSKDHVFPVNDG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FQALQGIIHSILKKS 179
                                          11.6%;
                                          Score 113; DB 2;
Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coiled coil; extracellular matrix; glycoprotein; trime
    Mismatches
    , 08
                                                                                Length 1747;
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    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             < VWA1 >
20;
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                                                                                                                                                                                                                                                                                                                           < VWA2 >
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Gaps
    11;
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DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 57

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RESULT 10
S31212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revis)
C;Accession: S31212
R;Waelchli, C;; Trueb, J;; Kessler,
 collagen alpha 1(XIV) chain precursor,
C;Species: Gallus gallus (chicken)
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A; Residues: 1-1857 <WAE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen alpha 1(XIV) chain precursor, short form - chicken
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
                                        S78476
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                                                       RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S31212
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                          1213 DELITFVC 1220
                                                                                                                                                                                                                                                         1102 TKETLLEAIQQI--AYKGGNTKTGKAIKHARE-VLFTGEAGMRKGIPKVLVVITDGRSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        986
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                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                HSILKKSC 180
                                                                                                                                                                                                                     DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII
                                                                                                                                                                                                                                                                                           DREQIROGLEELOKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE
                                                                                                                                                                                                                                                                                                                                DLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTEFKLNAYK 1101
                                                                                                                                                                                                                                                                                                                                                                    DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFFVNDGFQALQGII 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKETLLEAIQQI--AYKGGNTKTGKAIKHARE-VLFTGEAGMRKGIPKVLVVITDGRSQD 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DV-----NKVSREMQLDGFSFFAIGVADADYSELVNIGSKPSERHVFFVDD-FDAFTKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DV----NKVSREMQLDGFSFFAIGVADADYSELVNIGSKPSERHVFFVDD-FDAFTKIE 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DREQIROGLEELOKVLPGGDTYMHEGFERASEQIYYENROGYRTA--SVIIALTDGELHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212, 483-490, 1993
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
gallus
                                                                                                                                                                                                                                                                                                                                                                                                    11.6%; Score 113; DB 2; Length 1857;
26.1%; Pred. No. 0.25;
tive 39; Mismatches 80; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B.; Winterhalter, K.H.; Trueb,
                 long
                   form
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                   chicken
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F;39-110/Domain: fibronectin type III repeat homology <FN3B>
F;352-433/Domain: von Willebrand factor type A repeat homology <V
F;352-433/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3D>
F;534-614/Domain: fibronectin type III repeat homology <FN3B>
F;623-707/Domain: fibronectin type III repeat homology <FN3F>
F;741-823/Domain: fibronectin type III repeat homology <FN3F>
F;922-1009/Domain: fibronectin type III repeat homology <FN3F>
F;922-1009/Domain: fibronectin type III repeat homology <FN3H>
F;1040-1205/Domain: fibronectin type III repeat homology <FN3H>
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A;Residues: 1-416;1460-1811,1843-1888
A;Cross-references: EMBL:X70793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-1888 <TRUS
A;Cross-references: UNIPROT:P32018;
R;Waelchli, C.; Trueb, J.; Kessler,
Eur. J. Biochem. 212, 483-490, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Complete primary structure of chicken collagen A; Reference number: S31211; MUID: 93185668; PMID: 8444186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: Coll4A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: S78476;
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1213 DELITFVC 1220
                                                                                                                                                                                                                                                                                                                                          1042 DLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTEFKLNAYK 1101
                                                                                                                                                                                                                          1102 TKETLLEAIQQI--AYKGGNTKTGKAIKHARE-VLFTGEAGMRKGIPKVLVVITDGRSQD
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49; Conserv
                                                       HSILKKSC
                                                                                                               DV----NKVSREMQLDGFSFFAIGVADADYSELVNIGSKPSERHVFFVDD-FDAFTKIE 1212
                                                                                                                                                                  DLFFYSEREANRSRDL-GAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 172
                                                                                                                                                                                                                                                                               DREQIRQGLEELOKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 113; DB;
; Pred. No. 0.25;
39; Mismatches
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RESULT 12
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BHHU

Complement factor B precursor [validated] - human

complement factor B precursor [validated] - human

N;Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; heat-l

N;Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragment

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Accession: S34075, A44622; A00934; A19188; A19947; B19947; B25971; S14339; A44628; I544

C;Accession: S34075, A44622; A00934; A19188; A19947; B25971; S14339; A44628; I544

R;Mejia, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G.

submitted to the EMBL Data Library, March 1993

A;Accession: S34075

A;Accession: S34075

A;Accession: S34075

A;Accession: S34075

A;Accession: S34075

A;Accession: S34075

A;Accession: S34075

A;Accession: S34075

A;Cobs-references: UNIPROT:P00751; EMBL:X72875; NID:g297568; PIDN:CAA51389.1; PID:g29756

A;Cobs-references: UNIPROT:P00751; EMBL:X72875; NID:g297568; PIDN:CAA51389.1; PID:g29756

A;Title: Isolation of cDNA clones for the human complement protein factor B, a class III

A;Title: Isolation of cDNA clones for the human complement protein factor B, a class III
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A;Molecule type: mRNA
A;Residues: 339-509 <CAl>
A;Residues: GB:G00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
A;Cross-references: GB:G00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
A;Wu, L.; Morley, B.J.; Campbell, R.D.
Cell 48, 331-342, 1987
Cell 48, 331-342, 1987
A;Title: Cell-specific expression of the human complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: evidence and complement protein factor B gene: ev
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 16-225,'F',227-259 <MOR>
A;Residues: 16-225,'F',227-259 <MOR>
A;Residues: 16-225,'F',227-259 <MOR>
R;Schwaeble, W.; Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche Immunobiology 188, 221-232, 1993
A;Title: Human complement factor B: functional properties of a recombinant zymogen of th A;Reference number: I54409; MUID:94041399; PMID:8225386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Internal homologies of the Ba fragment from human A;Reference number: A44628; MUID:84158524; PMID:6323161 A;Accession: A44628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 270-329 <NIE>
A;Note: binding site for carbohydrate to lysine
R;Morley, B.J.; Campbell, R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. J. 274, 473-480, 1991
A;Title: The principal site of glycation of human complement
A;Reference number: S14339, MUID:91174758; PMID:2006911
A;Accession: S14339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-99 <WUL>
A;Residues: 1-99 <WUL>
A;Cross-references: GB:M15082; NID:g187699; PIDN:AAA59625.1;
R;Niemann, M.A.; Bhown, A.S.; Miller, E.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Campbell, R.D.; Porter, R.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983
A;Title: Molecular cloning and characterization of the A;Reference number: A19947; MUID:83273641; PMID:6308626
A;Accession: A19947
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A/Title: Amino acid sequence of the Bb fragment from complement factor B. Sequence of A/Reference number: A19188; MUID:83204002; PMID:6342610
A/Reference the final paper in a series documenting the sequence, glycosylation site,
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A/Note: the authors translated the codon TAC at 519 as Thr; t
R/Mole, J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.E.
J. Biol. Chem. 259, 3407-3412, 1984
A/Title: Complete primary structure for the zymogen of human
A/Reference number: A20751; MUID:84161997; PMID:6546754
                                       A;Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; PID:g4261689 R;Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Pujita, S.; Volanakis, Mol. Immunol. 30, 1587-1592, 1993
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A; Residues: 346-764 < CAM>
                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-764 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO J. 3, 153-157, 1984
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A,Residues: 260-296,'T',298-764 <CHR>
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A; Residues: 26-764 < MOL>
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cDNA cloning, nucleotide sequencing, phenotypic conv
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C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; v C;Reywords: acute phase; complement alternate pathway; duplication; glycoprotein; hydrol P;1-25/Domain: signal sequence #status predicted <SIG>
F;26-764/Product: complement factor B #status experimental <MAT>
F;26-259/Product: complement factor B #status experimental <BAF>
F;37-98/Domain: complement factor H repeat homology <FH1>
F;103-158/Domain: complement factor H repeat homology <FH2>
F;165-218/Domain: complement factor H repeat homology <FH3>
F;260-764/Product: C3/C5 convertage Bb fragment #status experimental <BBF>
F;268-458/Domain: von Willebrand factor type A repeat homology <FFA>
F;37-76,62-98,103-145,131-158,165-205,191-218,478-596,511-527,599-615,656-682,695-725/Di
F;122,142,285,378/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;259-260/Cleavage site: Arg-Lys (complement factor D) #status experimental
F;526,576,699/Active site: His, Asp, Ser #status experimental
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A;Molecule type: mRNA
A;Residues: 1-31,'Q',33-764 <RE2>
A;Cross-references: GB:L15702; NID:g291921;
C;Comment: 292-Cys has a free sulfhydryl.
C;Genetics:
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A; Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; A; Note: the list of introns may be incomplete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
439 INALASKKONEQHVFKVKD-MENLEDVFYQMIDES 472
                                                                                                                                                                                        100
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                                                                                                                                                                                                                                                    325 SEADSSNADWVTKQLNEINYEDHKLKSGTNT-----KKALQAVYSMMSWPDDVPPEGWN 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                           ETQLARIADSKDHVFPVNDGFQALQGIIHSILKKS 179
                                                                                                                                                                                                                                                                                                                                                                                 GSMNIYLVLDGSDSIGASNFTGAKKCLVNLIEKVASYGVKP--RYGLVTYATYPKIWVKV 324
                                                                                                                                                                                                                                                                                                                                                                                                                                             GGFDLYFILDKSGSV-----LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKL 55
                                                                                                                          RTRHVIILMTDGLHNMGGDPITVIDEIRDLLYIGKDRKNPREDYLDVYVFGVGPLVNQVN 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 111.5; DI
Pred. No. 0.11;
4; Mismatches
                                                                                                                                                                                     ----ELHEDLFFYSEREANRSRDLGAIVYCVG--VKDFN 144
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R;Wei, Y.; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
Dev. Biol. 168, 503-513, 1995
A;Title: Monoclonal antibody MT2 identifies the urodele
A;Reference number: I51027; MUID:95246925; PMID:7729585
A;Accession: I51027
                                                                                                                                                                                                                                                                                                  C; Accession: I51027
R; Wei, Y.; Yang, E.
                                                                                                                                                                                                                                                                                                                                                                                               type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
A;Cross-references: UNIPROT:Q91145; EMBL:U19494; NID:g632647; F;155-236/Domain: fibronectin type III repeat homology <3FR>
                                                                 A; Residues: 1-929 <WEI>
                                                                                             A; Molecule type: mRNA
                                                                                                                               A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I51027
                                                                                                                                                                                                                                                                                                                                                             Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                   from GB/EMBL/DDBJ
                                                                                                                                                                                                                                alpha
                                                                                                                                                                                                                                    chain
                                                                                                                                                                                                                                of type XII collage
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PIDN: AAA80217.1; PID: 963264

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Octlagen alpha 1(VII) chain precursor - human

(C.Species: Homo sapiens (man)

C.Species: Local (man)

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A.Reference number: A54849; MUID:9427589; PMID:8051117

A.Accession: A54849

A.Accession: A54849

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                                                        R;Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E. J. Biol. Chem. 264, 3822-3826, 1989
A;Biol. Chem. 264, 3822-3826, 1989
A;Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagena A;Reference number: A30296; MUID:89139437; PMID:2537292
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N;Alternate names: procollagen alpha 1(VII) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ঠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;631-795/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   806 TENVC 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 633 DIVLLVDGSWSIGRPNFKIVRNFISRVVEVFDIGSDRVQIAVSQYSGDPRTEWQLNTHKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        750 IVAPSKRYA----DEGIELYAVGIKNADENELKEIASDPDELYMYNVADFSLLTNIVNDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 11.5%;
Similarity 23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKKSC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVN-DGFQALQGIIHSI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKSLMDAVANLPYKGGNTNTGSALKFILENNF---RPGVGMREKARKIAILLTDGKSQDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGY----RTASVIIALTDGELHED
      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 111.5; D
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: two reported R;Greenspan, D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: COL7A1; EBR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
      174
                                                               154
                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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F;1170-1172/Region: cell attachment (R-G-D) motif
F;1189-1253/Region: cysteine/proline-rich
F;1254-2783/Region: cysteine/proline-rich
F;1234-1336/Region: cill attachment (R-G-D) motif
F;1334-1336/Region: cell attachment (R-G-D) motif
F;2008-2010/Region: cell attachment (R-G-D) motif
F;2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;337,786,1109/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;3167,2176,2185,2189,2664,2667,2673/Modified site: 4-hydroxypyroline (Pro) #s
F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;2634,2802,2804/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;231-318/Domain: fibronectin type III repeat homology <FN1>
F;327-413/Domain: fibronectin type III repeat homology <FN2>
F;414-502/Domain: fibronectin type III repeat homology <FN2>
F;508-593/Domain: fibronectin type III repeat homology <FN4>
F;598-683/Domain: fibronectin type III repeat homology <FN5>
F;598-683/Domain: fibronectin type III repeat homology <FN5>
F;686-771/Domain: fibronectin type III repeat homology <FN6>
F;76-862/Domain: fibronectin type III repeat homology <FN8>
F;864-952/Domain: fibronectin type III repeat homology <FN8>
F;954-1045/Domain: fibronectin type III repeat homology <FN8>
F;1052-1219/Domain: von Willebrand factor type A repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: structural component of extracellular polymer associated with anchoring fi C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprolir F;1-16/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 3p21.3-3p21.3

A;Note: defects in this gene can result in dominant and recessive dystrophic epidermolyst A;Note: there are 118 introns
C;Complex: type VII collagen is probably a homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:L06862; NID:g388713; PIDN:AAA89196.1; PID:g388714
R;Christiano, A.M.; Ryynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly A;Reference number: A55255; MUID:94224777; PMID:8170945
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F_117-1253/Domain: amino-terminal nonhelical #status predicted F_136-201/Domain: von Willebrand factor type A repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C_fComment: Prolines and lysines at the third position of ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 2395-2871, 'S', 2873-2944 < RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: The carboxyl-terminal half of type VII collagen, A; Reference number: I48103; MUID:93271985; PMID:8499916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;'I;Note: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genet. 2, 273-278, 1993
                                                                              116 DLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIH
                                                                                                                                                                 98 GSGGDVIR-AIRELS--YKGGNTRTGAAILHVADHVFLPQLARPGVPKVCILITDGK-SQ 153
                                                                                                                                                                                                                                           56 TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHE
                                                                                                                                                                                                                                                                                                                                      38 DIVFLLDGSSSIGRSNFREVRSFLEGLVLPFSGAASAQGVRFATVQYSDDPRTEFGLDAL
                                                                                                                                                                                                                                                                                                                                                                                                                 4 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF---ISPQ-LRMSFIVFSTRGTT---LMKL
DLV---DTAAQRLKGQGVKLFAVGIKNADPEELKRVASQPTSDFFFFVND-FSILRTLLP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EBR1; EBD1; EB
GDB:128750; OMIM:120120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 110; DB 2; Length 2944; Pred. No. 0.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / <FN9>
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the tripeptide repeating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the non-collagenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                  173
                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #status experi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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A/Title: Structure of cDNAs encoding the triple-helical domain of murine alpha-2(VI) col rate oligonucleotides for generation of novel cDNA clones.

A;Reference number: $13745

A;Reference number: $13745

A;Reference number: $13745

A;Residues: $26-267,'S',269-294,'L',296-600 <CON>
A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192672

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192672

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192672

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192672

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192672

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192672

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192672

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192672

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192672

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192672

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192671

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192671

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192671

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192671

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192671

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192671

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192671

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192671

A;Cross-references: GB:L06343; NID:g192671; PIDN:ARA37441.1; PID:g192671

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A;Residues: 1-1029 <IBR>
A;Cross-references: UNIPROT: (002788; EMBL:X65582; NID:g49808; PIDN:CAA46541.1; PID:g49809
A;Cross-references: UNIPROT: (002788; EMBL:X65582; NID:g49808; PIDN:CAA46541.1; PID:g49809
A;Cross-references: UNIPROT: (002788; EMBL:X65582; NID:g49808; PIDN:CAA46541.1; PID:g49809
Biochem. J. 289, 141-147, 1993
Biochem. J. 289, 141-147, 1993
A;Title: Cloning of alpha2 chain of type VI collagen and expression during mouse develop A;Reference number: S28808; MUID:93143659; PMID:8380980
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Q6dfx2 mus musculu
Q8bvm2 mus musculu
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bMed-14702039; DOI=10. A T., SUZUKÍ Y., NISHÍI kamateu A., Hayashi K., kirat M., Obayashi M., umamorco JI., Saito K., ugahari K., Murakami K. ugahari K., Murakami K. ugahari K., Murakami K. ugahari K., Murakami K. ugawara M., Takahashi M. unazaki M., Ninomiya K. ujimori K., Tanai H., K. unijimori K., Tanai H., K. unazaki M., Wasashino K. onge N., Musashino K. onge N., Musashino K. unazaki H., Watanaba K. unazaki H., Watanabe T. unazaki M., Watanabe T. unazaki M., Watanabe T. unazaki M., Watanabe T. unadak K., Fujii wabata A., Hikiji T., titani R., Kawakami T.,	RESULT 1 ATRI HUMAN STANDARD; P. ATRI HUMAN STANDARD; P. AC Q946X2; Q96P02; Q9NVP3; DT 28-FEB-2003 (Rel. 41, Created) DT 28-FEB-2003 (Rel. 44, Last sequ DT 05-JUL-2004 (Rel. 44, Last sequ DT 05-JUL-2004 (Rel. 44, Last sequ DT 05-JUL-2004 (Rel. 44, Last sequ DT 05-JUL-2004 (Rel. 44, Last sequ DT 05-JUL-2004 (Rel. 47, Last sequ DT 05-JUL-2004 (Rel. 47, Last sequ DT 05-JUL-2004 (Rel. 47, Last sequ DT 05-JUL-2004 (Rel. 47, Last sequ DE Name-ANTXR1; Synonyms-ATR, TEMB OS Homo sapiens (Human). CC Eukaryota; Metazoa; Chordata; C OC Mammalia; Eutheria; Primates; C OC Mammalia; Eutheria; Primates; C OX NCBI_TaxID=9606; RN [1] RN SEQUENCE FROM N.A. (ISOFORM 1). RX MEDLINE=20407466; PubMed=109479 RA Kinzler K.W.; RT "Genes expressed in human tumor RL Science 289:1197-1202(2000). RN [2] RP SEQUENCE FROM N.A. (ISOFORM 2). RX MEDLINE=21557240; PubMed=117005 RA Bradley K.A., Mogridge J., Mour RT "Identification of the cellular RL Nature 414:225-229(2001). RP SEQUENCE OF 184-564 FROM N.A. (ISOFORM 3).	32 116 12.0 637 2 Q 33 116 12.0 1284 2 Q 34 116 12.0 1329 1 K 35 116 12.0 2944 2 Q 36 116 12.0 3183 2 Q 37 116 12.0 3783 1 M 39 114.5 11.8 2104 2 Q 40 113.5 11.7 790 2 Q 41 113.5 11.6 599 2 Q 41 113.1 11.6 599 2 Q 42 112.5 11.6 1347 2 Q 44 112.5 11.6 1347 2 Q 45 112.5 11.6 1347 2 Q
O.1038/ng1285; hikawa T., Otsuki T., Sugiyama T., Irie R., K., Sato H., Nagai K., Kimura K., Makita H., Nishi T., Shibahara T., Tanaka T., Ishii S., K., Kawai Y., Isono Y., Nakamura Y., K., Kawai Y., Isono Y., Nakamura Y., K., Kawai Y., Isono Y., Nakamura Y., M., Kawai Y., Isono Y., Nakamura Y., M., Kanda K., Yokoi T., Furuya T., Kikkawa E., hara K., Katsuta N., Sato K., Tanikawa K., K., Ishibashi T., Yamashita H., Murakawa K., K., Ishibashi T., Yamashita H., Murakawa K., K., Ishibashi T., Yamashita H., Murakawa K., K., Kanata M., Watanabe M., Hiraoka S., Chiba Y., Ishibashi T., Yamashita H., Tanase TO., Kimata M., Watanabe S., Yosida M., Hotuta T., Takahashi-Fujii A., Hara H., Tanase TO., Kommai F., Hara R., Takeuchi K., Arita M., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yuuki H., Oshima A., Sasaki N., Aotsuka S., Yuuki H., Oshima A., Sasaki N., Sano S., Satoh N., Takami S., Terashima Y., Suzuki O., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., T., Sugiyama A., Takemoto M., Kawakami B., K., Kumaggai A., Itakura S., Fukuzumi Y., K., Kumaggai A., Itakura S., Fukuzumi Y., K., Kumaggai A., Itakura S., Fukuzumi Y., K., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,	ed) sequence update) annotation update) ecursor (Tumor endothelial marker 8). TEM8; a; Craniata; Vertebrata; Euteleostomi; s; Catarrhini; Hominidae; Homo. 1). 947988; DOI=10.1126/science.289.5482.1197; lescu V., Traverso G., Romans K.E., ins G.J., Lengauer C., Vogelstein B., umor endothelium."; . 2), AND INTERACTION WITH ANTHRAX TOXIN. 700562; DOI=10.1038/n35111998; MOUREZ M., Collier R.J., Young J.A.T.; ular receptor for anthrax toxin.";	QBIVX1 QBivx1 homo sapien QBPIS9 QSPIS9 homo sapien QBPIS9 QSPISI homo sapien QBSB70 QSB718 homo sapien QBSZC2 QBSZC2 caenorhabdi MIA3 CAEEL Q34576 caenorhabdi Q21281 Q21281 caenorhabdi Q264N4 Q964n4 caenorhabdi Q964N6 Q964n4 caenorhabdi Q964n4 Q961281 caenorhabdi Q6CQ6 Q8mvq1 QBMVQ1 Q964n4 caenorhabdi QBCQ6 Q8mvq1 boltenia vi QALE CHICK Q8mvq1 boltenia vi QBC272 Q811us gallus gal

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RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Pahey J., Helton E., Ketteman M., Madan A., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Tennence M., Schein J.E., Jones S.J.M., Marra M.A.,
Tennence M., Schein J.E., Jones S.J.M., Marra M.A.,
Tennence M., Schein J.E., Jones S.J.M., Marra M.A.,
Tennence M., Schein J.E., Jones S.J.M., Marra M.A.,
Tennence M., Schein J.E., Jones S.J.M., Marra M.A.,
Tennence M., Schein J.E., Jones S.J.M., Marra M.A.,
Tennence M., Schein J.E., Jones S.J.M., Marra M.A.,
Tennence M., Schein J.E., Jones S.J.M., Marra M.A.,
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Hillman R.T., Green R.E., Brenner S.E.;
"An unappreciated role for RNA surveillance.";
Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22608610; PubMed-12700348; DOI=10.1073/pnas.0431098100; Scobie H.M., Rainey G.J.A., Bradley K.A., Young J.A.T.; "Human capillary morphogenesis protein 2 functions as an anthra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satch T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
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                                                                                                                                                        but not in n
DOMAIN: Bind
SIMILARITY:
                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELIULAR LOCATION: Type I membrane protein ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named 1soforms=4;
Comment=Experimental confirmation may be law
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis. Binding does not occur in the presence of calc
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SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q9H6X2-1; Sequence=Displayed;
Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9H6X2-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9H6X2-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9H6X2-2; Sequence=VSP_000444,
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                                                                                                                                                   SPECIFICITY: Highly expressed in tumor endothelial of in normal endothelial cells.

Binding to PA seems to be effected through the VWA
ITY: Belongs to the ATR family.

ITY: Contains 1 VWFA domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence=VSP_000446,
                                                                                                                                                                                                                                                                                                                                                             Sequence=VSP_000448,
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Matches 187
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InterPro; IPR008399; Ant C.
InterPro; IPR002035; VWF A.
Pfam; PF05587; Anth Ig; I.
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                                                                                           SEREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSC
                                                                                                                                             QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
                                                                                                                                                                  QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFY
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Pred. No. 2.1e-74;
; Mismatches 0;
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RESULT 2
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STANDARD;

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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojbbori T.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojbbori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gassterland T., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Verardo R., Wangher L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Miyazaki T., Wahi K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Masunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Masunishi A., Sasaki Y., Basaki D., Sihbata R., Shinagawa A.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Masunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Minaishi A., Sasaki Y., Basaki D., Shinagawa A.,
RA Hara A., Hashizume W., Imaterston R., Lander E.S., Rogers J.,
RA Hara A., Hashizaki Y.,
RA Hara A., Hashizaki Y.,
RA Hara A., Hashizaki Y.,
RA Hara A., Hashizaki Y.,
RA Hara A., Hashizaki Y.,
RA Hara A., Katanaba R., Sataki M., 
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28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60,770 full-length cDNAs.";

Nature 420:563-573(2002).

-i- FUNCTION: Cellular role is not yet known.

-i- SUBUNIT: Binds to the protective antigen (PA)

anthracis (By similarity).

-i- SUBCELLULAR LOCATION: Type I membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Createu, 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 05-JUL-2004 (Rel. 44, Last annotation update) Anthrax toxin receptor 1 precursor (Tumor endothelial marker Anthrax toxin synonyms=Atr, Tem8;
                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=21443268; PubMed=11559528;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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                               ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
ified and this statement is not removed. Usage by and for com
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Event=Alternative spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9CZ52-1;
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                                                                                                                                                                                                                                                                                                                                             Bimilarity
and this statement is not removed. Usage by and for commercia. requires a license agreement (See http://www.isb-sib.ch/announce.
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                                                                                                                                                                                                                                                              Contains 1 VWFA domain.
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Best Local
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InterPro; IPR008399; Ant C.
InterPro; IPR002035; VWF A.
Pfam; PF05587; Anth IG; I.
Pfam; PF05586; Ant_C; I.
Pfam; PF00586; Ant_C; I.
Pfam; PF00092; VWA; I.
PROSITE; PS50234; VWFA; I.
                                                                                                                                                                                                                                                                                         ATRZ HUMAN STANDARD; PRT; 489 AA P58335, Q86UI1; Q8NB13; Q96NC7; 28-FEB-2003 (Rel. 41, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation updat Anthrax toxin receptor 2 precursor (Capilla
                                                                                                                                                                                                                                                                                                                                                                                                                                          MAMUH
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TRANSMEM
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VARSPLIC
Bell S.B., Mavila A., Salazar R., Bayless K.J., Kanagala S., Maxwell S.A., Davis G.E.;
"Differential gene expression during capillary morphogenesis collagen matrices: regulated expression of genes involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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DOMAIN
                                                                                                                                                                                      Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                         SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=21539596; PubMed=11683410;
                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                        Name=ANTXR2; Synonyms=CMG2;
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MGD; MGI:1916788; Antxr1
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                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                  (CMG-2)
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splicing; G
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Pred. No. 1.2e-73
1; Mismatches
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N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
GRCINFTCWASQPAKYPLNNTYHPSSPPDAPIYTPPPPPAPHCPPPAPHTPPIFSSPPSTLPPPPQAPPPRAPPPSRPPPRPSV -> RFRGWRLTICLGSKHVHDDDNNTYTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rotein; Receptor; Signal; Transmembrane.
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Pro-rich.
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                                                                                                                                                                                                                                                                                                   ion update)
(Capillary
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa M.,
RA Tujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Noriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fukuzumi Y.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fukuzumi Y.,
RA Kawabata A., Hikiji T., Kobatake N., Itagaki H., Ikema Y., Okamoto S.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Masaho Y., Vamashita R.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Makashi Y., Nakagawa K.,
RA Nakajawa K., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA Nakai Y., Matanaki K., Matanaka K., Matanaka M., Matanaka K.,
RA Nakagasa T., Namura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane matrix assembly, cell cycle progression, differentiation and G-protein signaling.";
J. Cell Sci. 114:2755-2773(2001).
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PubMed=14702039; DOI=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Cellular role is not yet known. (PA) of Bacillus SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis in a divalent cation-dependent manner, with the following preference: calcium - manganese - magnesium - zinc. Seems to bind to collagen type IV and laminin. SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2). Secreted (isoform 3). Isoform 1 is expressed at the cell surface while isoform 2 is predominantly expressed within the endoplasmic
liver, peripheral blood leukocy small intestine and spleen.

DOMAIN: Binding to PA seems to SIMILARITY: Belongs to the ATR
                                                                                                                                               Note=No experimental TISSUE SPECIFICITY: Exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCE Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genet.
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                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P58335-2;
                                                                                                                                                                                                                          IsoId=P58335-4; Sequence=VSP_008346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P58335-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ھ
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                                                                                                                peripheral blood leukocytes,
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                                                                                                                                                                                                                                                                                                     experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                 Sequence=VSP_008344, VSP_008
ental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence=Displayed,
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence=VSP_008343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          splicing; Named isoforms=4;
                                                                                                                                                  Expressed in colon, heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100:5170-5174 (2003)
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                                         through the VWA domain
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Q6DFX2;
25-OCT-2004
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                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                  ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                    REANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIE
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                                               PRELIMINARY;
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AAP04016.1;
BAB70976.1;
BAC03731.1;
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TLDVSVSFNGGKSVISGSLIVTATECSNGIAAI
VTQAGVKWHDLTHCTFGLSGSGDPPTSAS (in
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P -> A (in Ref. 3;
B9F679DB75B6E2B7
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                                                PRT;
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A Strausborg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,

A Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Stapleton M., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratte P.H.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Mithing M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,

Karywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Kornes G. T. Maxra M. A., Schmutz J., Myers R.M., Schein J.E.,

Kornes G. T. Maxra M. A., Schmutz J., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 109
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO08400; Anth Ig.
InterPro; IPRO0839; Ant C.
InterPro; IPR002035; WMF A.
Pfam; PP05587; Anth Ig; I.
Pfam; PP05586; Ant C; 1.
Pfam; PP00992; WMA; 1.
 Q8BVM2,
                                                                                                                                                                                                                                                                                                          Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases. EMBL, BC076595; AAH76595.1; -. EMBL, GO:0016021; C:integral to membrane; IEA. GO: GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6; TI
MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

CTBAIN=C57BL/6; TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Generation and initial analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                            IL 184
                                                                                                                                                                                                                                                                                                       487 AA;
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              PRELIMINARY;
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TISSUE-Eye;
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Pred. No. 2e-38;
2; Mismatches
             PRT;
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SEQUENCE FROM N.A.
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carrinci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                      Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P. Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hari F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takada Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Testis;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwaji K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwaji K.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sanotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933430J11 product:hypothetical Proline-rich reg:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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TISSUE=Testis;
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Mammalia; Eutheria;
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Nature 409:685-690(2001).
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Sciurognathi; Muridae;
   IEA
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Sano Tagami /
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InterPro; IPR008400; Anth Ig.
InterPro; IPR002035; VWF Ā.
Pfam; PF05587; Anth_Ig; Ī.
Pfam; PF00952; VWA; Ī.
PFRINTS; PR00453; VWFADOMAIN.
SMART; SM00327; VWA; I.
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01-JUN-2001
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            PROSITE; PS50234; VWFA; 1.
Cell adhesion; Integrin; Signal; Transmembrane.
SIGNAL 1 30 Potential.
SIGNAL 1 30 Potential.
                                                                                                  SMART;
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolldobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                               InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Immunol. 166:1710-1715(2001).
-!- SUBCELLULAR LOCATION: Type I membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miyazawa S., Azumi K., Nonaka M.; "Cloning and characterization of integrin alpha subunits from the solitary ascidian, Halocynthia roretzi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-UN-2001 (TYEMBLrel. 17, Created)
01-UN-2001 (TYEMBLE). 17, Last sequence update)
01-UN-2003 (TYEMBLE). 24, Last annotation update)
Integrin alpha Hrl precursor:
                                                                                                                                              PRINTS; PRO1185; INTEGRINA. PRINTS; PRO0453; VWFADOMAIN.
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MEDLINE=21103187; PubMed=11160215;
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GO:0008305; C:integrin complex; IEA.
GO:0005515; F:protein binding; IEA.
GO:0007516; P:cell-matrix adhesion; IEA.
GO:0007229; P:integrin-mediated signaling pathway; IEA.
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                                                                                               SM00191; Int_alpha; 5.
SM00327; VWA; 1.
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Bithe European Bioinformatics Institute. There are no restiuse by non-profit institutions as long as its content use by non-profit institutions as long. As its content use by non-profit institutions as long. As its content use by non-profit institutions as long.
                                                                                                                                                                                                                                                  borne pathogens, particulate matter, and senescent erythrocyt from the blood (By similarity).

-i- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).
-i- SUBCELLULAR LOCATION: Type I membrane protein (By similarity) bowalin. The integrin I-domain (insert) is a VWFA domain. Integrin Location in the standard classer of the standard contains of the integrin alpha chain family.
-i- SIMILARITY: Contains 1 FG-Gap repeats.
-i- SIMILARITY: Contains 1 VWFA domain.
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         InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VMF A.
Pfam; PF01839; FG-GAP; 3.
Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
                                                                                    EMBL; AF021334; AAF21241.1; -. HSSP; P11215; 18HQ.
                                                                                                                                or send an email to license@isb-sib.ch)
                                                                                                                                                entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley;
O'Brien M.M., VanderVieren M., Kilgannon P.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116
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to the EMBL/GenBank/DDBJ databases.
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34; Mismatches
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Q8T6U5 PRELIMINARY; PRT; 441 AA.
Q8T6U5;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Proximal thread matrix protein 1 variant a.
Mytilus edulis (Blue mussel).
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PROSITE; PS50234; VWFA; 1.
Calcium; Cell adhesion; Glycoprotein; Integrin; Magnesium; Receptor;
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SM00327; VWA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 141.5;
Pred. No. 0.00
38; Mismatches
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Extracellular (Potential).
Potential.
(Ytoplasmic (Potential).
FG-GAP 1.
FG-GAP 2.
VWFA.
FG-GAP 3.
FG-GAP 4.
FG-GAP 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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Best Local
          Query Match
Best Local S
                                                 PRINTS; PRO0453; VWFADOMAIN
SMART; SM00327; VWA; 2.
PROSITE; PE50234; VWFA; 2.
Matrix protein.
SEQUENCE 444 AA; 47815 M
                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903;
Sun C., Lucas J.M., Waite J.H.;

"Collagen-binding matrix proteins from elastomeric extrace byssal fibers.";
                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
                                                                                                                 EMBL, AY053390; AAL17973.1; -. GO; GO:0005198; F:structural molecule activity; IEA. InterPro; IPR002035; VWF_A. Pfam; PF00092; VWA; 2.
                                                                                                                                                                                                                                                                           Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                  Q8T5C3
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SMART; SM00327; VWA; 2.
PROSITE; PS50234; VWFA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomacromolecules 3:1240-1248(2002).
EMBL; AF414454; AAL83537.1; -.
GO; GO:0005198; F:structural molecul
InterPro; IPRO20335; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903; Sun C., Lucas J.M., Waite J.H.;
                                                                                                                                                                      Biomacromolecules 3:1240-1248(2002).
                                                                                                                                                                                                                                                                                                                 Proximal thread matrix protein 1b.
                                                                                                                                                                                                                                                                                                                                                                    Q8T5C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matrix protein.
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Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                             NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00092; VWA; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Collagen-binding matrix proteins
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 50;
              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLTDGQNNGHKS----PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-TTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTDGEL--HEDLFFYSERBANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPVND 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLTE--DREQIRQGLEELQKVLPG--GDTYMHEGFERASEQIYYENRQG---YRTASVII 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGFDLYFILDKSGSV----LHHWNBIYYFVEQLAHKF--ISPQ-LRMSFIVFSTRGTTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFNKLSKIMENVVKLACM 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFQALQGIIHSILKKSCI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHADIAFVFDASSSINANNPNNYGLŃKDFMKDIVDRFNKTGPDGTQFAVVTFADRATKQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441 AA; 47543 MW;
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                     47815 MW;
            14.5%;
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                                                                                                                                                                                                                                                                                                                          21, Created)
21, Last sequence update)
24, Last annotation update)
 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46; Mismatches
Score 141; DB 2
Pred. No. 0.001;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 141; DB 2
Pred. No. 0.001;
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                                                   D2C605347450C931 CRC64;
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                                                                                                                                                                                                elastomeric extraorganismic
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                                                                                                                                                                                                                                                                                         Pteriomorphia; Mytiloida;
                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                   8
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  76;
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                        Length 444;
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  Indels
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 26;
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CA1C MOUSE STANDARD

Q6087; P70322;

15-JUL-1998 (Rel. 36, C

28-PEB-2003 (Rel. 41, I

25-OCT-2004 (Rel. 45, I

Collagen alpha 1(XII) c
                                                                                                                                                                              Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R.W., Olsen B.R., Nishimura I.,
"Structural variation of type XII collagen at its carboxyl-terminal NC1 domain generated by tissue-specific alternative splicing.";
J. Biol. Chem. 274:22053-22059(1999).
-i- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrillar matrix (By similarity).
-i- SUBBUNIT: Trimer of identical chains each containing 190 kDa of
                                                                                                                                                                                                                                                                                                                                                              collagen XII and their tissue-specific expression during development.":
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96170761; PubMed=8601036;
Boehme K., Li Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and sho
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                                                                                                                                                                                                                                                                               MEDLINE=99348349; PubMed=10419532; DOI=10.1074/jbc.274.31.22053;
Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R
                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Skin fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Coll2al;
                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           development
                                                                                                                                                                                                                                                                                                                                                                                                                          XIIB-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
ISOId=Q60847-4; Sequence=VSP_001150, VSP_001151, VSP_001152; TISSUE SPECIFICITY: Highest expression in tendons, perichondrium skin, cornea, sclera, blood vessels, and periosteum. DEVELOPMENTAL STAGE: The long NC3 XIIA isoforms are predominant early stages (ED7 and 11); at later stages of development (ED15
                                                                                                       Name=XIIA-1; Sequence=Displayed;
                                                                                                                                                              nontriple-helical sequences (By similarity). ALTERNATIVE PRODUCTS:
                                                      Name=XIIB-2
                                                                                   Name=XIIA-2; Synor IsoId=Q60847-2;
                                                                                                                                        Event-Alternative splicing, Named isoforms=4;
Comment-The final tissue form of collagen X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357
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                                                                IsoId=Q60847-3;
                                                                                                                               homotrimers or any combination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LITDGQNNGHKS----PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-TTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLKDYSSKAEIKGAID---KVTPSIIGQTAIGDGLENARLEV-FPNRNGGGREEVQKVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHADI AFVFDASSSINANNPNNYGLMKD FMKDI VDRFNKTGPDGTQFAVVTFADRATKQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGFDLYFILDKSGSV----LHHWNEIYYFVEQLAHKF--ISPQ-LRMSFIVFSTRGTTLM
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                                                                                                                                                                                                                                                                                                                                               204:432-445(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             and Swiss Webster; TISSUE=Skin;
                                                                                              Synonyms=ER#K
                                                                                                                                                                                                                                                                                                                         FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   AND ALTERNATIVE
                                                              Sequence=VSP_001150;
                                                                                  Sequence=VSP_001151,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain precursor.
                                                                                                                                                                                                                                                                                                                           AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                          ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                               short splice variants
                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLICING (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3119 AA
                                                                                                                               of the
                                                                                   VSP_001152
                                                                                                                               various
                                                                                                                                                                                                                                                                                                                          SPLICING
                                                                                                                                       XII may contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi; 
Murinae; Mus
                                                                                                                               isoforms;
                                                                                                                                                                                                                                                                                                                          (ISOFORMS XIIA-2
                              VSP_001152;
perichondrium,
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and 17) the short NC3 XIIB forms become the major forms. As the short NC3 forms become the major product, the long splice variant continues to be expressed in several tissues, even after birth. The long NC1 isoforms, XIIA-1 and XIIB-1, peak in 15-day old embryos and decrease in 17-day old ones. The expression of the short NC1 form XIIB-2 remains constant throughout late stages of embryonic development (ED15 and ED17).

-i- pTM: The triple-helical tail is stabilized by disulfide bonds at each end (By similarity).
```

-i- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains (By similarity).

-i- PTM: O-glycosylation of isoform XIIA-2; glycosaminoglycan of

-!- PTM: O-glycosylation of isoform XIIA-2; glycosaminoglycan of chondroltin-sulfate type (By similarity).

-- SIMILARITY: Belongs to the fibril-associated collagens with interrupted helices (FACIT) family.

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InterPro; IPR008160; Collagen.
InterPro; IPR00895; ConA like_lec_
InterPro; IPR00895; FN III.
InterPro; IPR003961; FN III.-like.
InterPro; IPR003129; TSP N.
InterPro; IPR003129; TSP N.
InterPro; IPR002015; VWF A.
Pfam; PF01391; Collagen; 5.
Pfam; PF01391; Collagen; 5.
Pfam; PF00041; fn3; 18.
Pfam; PF00041; fn3; 18.
Pfam; PF00041; TSP N; 1.
Pfam; PF00092; VWA; 4.
                                                                                                                                                                                                                                              PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00260; FN3; 18.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 4.
PROSITE; PS50853; FN3; 18.
PROSITE; PS50334; VWFA; 4.
                                                                                                                                                                                                                    Glycoprotein; SIGNAL
                                                                                                                                                                                                                                        Alternative
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  splicing; Cell adhesion; Collagen;
n; Hydroxylation; Repeat; Signal; St
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                                                                                                                                                                                                           HEDLFFYSERBANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGI
                                                                                                                                                                                                                                                ----VEDIIKAINTPPYRGGSTNTGKAMTYVREKIFVPNK-GSRSNVPKVMILITDGE-
                                                                                                                                                                                                                                                                               QIRQGLEELQKVL-----PGGDTYMHEGFERASEQIYYENRQGYRT--ASVIIALTDGEL
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Nonhelical regions
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Pred. No. 0.015;
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O-linked (Xyl. . .) (chondroitin sulfate) (Potential).
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7; Mismatches
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Missing (In isoform XIIA-2 XIIB-2).
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EPY -> GSG (in isoform XIIB-2).
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N; 9B1F999C86AB3251 CRC64;
   PRT;
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MEDIINE=93149203; PubMed=8426611; DOI=10.1016/0166-6851(93)90255-V; Pasamontes L.E., Hug D., Huembelin M., Weber G.; "Sequence of a major Eimeria maxima antigen homologous to the Eimer: tenella microneme protein Etpl100."; Mol. Biochem. Parasitol. 57:171-174(1993). EMBL; M9905B; AAA29076.1; -
EMBL; M9905B; AAA29076.1; -
EIR; A48569; A48569.
HSSP; P07996; 1LSL.
GO; GO:0008083; F:growth factor activity; IEA.
InterPro; IPR000084; TSPI.
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
proximal thread matrix protein 1.
Mytilus galloprovincialis (Mediterranean mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                  Q04588;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY053391; AAL17974.1; -. HSSP; P20701; 1MJN. GO; GO:0005198; F: Btructural molecule
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                                                                                                                                                                    Major antigen homologous
Eimeria maxima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matrix protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50234; VWFA; 2.
Matrix protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0453; VWFADOMAIN. SMART; SM00327; VWA; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Collagen-binding matrix proteins from
byssal fibers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903; Sun C., Lucas J.M., Waite J.H.;
                                                                                                                                                                                                                                            NCBI_TaxID=5804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFDKLSKIMEDVVKLACM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTDGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFFVND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGFDLYFILDKSGSV----LHHWNEIYYFVEQLAHKF--ISPQ-LRMSFIVFSTRGTTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFQALQGIIHSILKKSÇI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLTDGQNNGHKS----PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-TTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLKDYSSKADIKGAID----KVSPSIIGQTAIGDGLENARLEV-FPNRNGGGREEVQKVVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLTE--DREQIRQGLEELQKVLPG--GDTYMHEGFERASEQIYYENRQG---YRTASVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHADIAFVFDASSSINANNPNNYQLMKNFMKDIVDRFNKTGPDGTQFAVVTFADRATKQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453 AA; 48784 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%;
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                                                                                                                                                                                                                                                                                                                          sequence (emp100).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                      724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity;
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                                                                                                                                                                                                                                                                                                                                          update)
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                                                                                                                                                                                                                                                                                       Eimeriidae;
                                                                                                                                                        the Eimeria
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Best Local S
Matches 53
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Pfam; PF00092; VWA; 1.

PRINTS; PR00453; UWFADOMAIN.

SMART; SM00209; TSP1; 6.

SMART; SM00327; UWA; 1.

PROSITE; PS50092; TSP1; 5.

PROSITE; PS50034; UWFA; 1.

SEQUENCE 724 AA; 75808 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P11215;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor Neutrophil adherence receptor).
Name=ITGAM; Synonyms=CD11B, CR3A;
                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-88257215; PubMed=2454931; DOI=1

Arnaout M.A., Gupta S.K., Pierce M.W.,

Arnaout M.A., Gupta S.K., Bierce M.W.,
                                                                                                                                                                                                                                                                          MEDLINE=88190151; PubMed=2833753;
Arnaout M.A., Remold-0'Donnell E., Pierce M.W., HArnaout M.A., Remold-0'Donnell E., Pierce M.W., H'Molecular cloning of the alpha subunit of human leukocyte adhesion glycoprotein Mol: chromosomal homology to the alpha subunits of integrins.";
Proc. Natl. Acad. Sci. U.S.A. 85:2776-2780(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type
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MEDLINE=93123748;
Fleming J.C., Pahl
                                                                                               Arnaout M.A., Gupta S.K., Pierce M.W., Tenen "Amino acid sequence of the alpha subunit of receptor Mol (complement receptor type 3).";
J. Cell Biol. 106:2153-2158(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88315033; PubMed=2457584;
Corbi A.L., Kishimoto T.K., Miller L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rbi A.L., Kishimoto T.K., Miller L.J., Springer T.A.; he human leukocyte adhesion glycoprotein Mac-1 (complement pe 3, CDILD) alpha subunit. Cloning, primary structure, and the integrins, von Willebrand factor and factor B."; Biol. Chem. 263:12403-12411(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNADILIAAAAKKI.PYAAGSTYTHI.GLAKA-EEII.FSFQKGGRDNAPKMII.VMTDGA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
  PubMed=8419480;
l H.L., Gonzalez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.1%;
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Pred. No.
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     U
                                                                                                                                                DOI=10.1083/jcb.106.6.2153;
M.W., Tenen D.G.;
subunit of human leukocyte
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"Experimental support for a beta-propeller domain in integrin alph subunits and a calcium binding site on its lower surface.";

Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875(1998).

-I- FUNCTION: Integrin alpha-M/beta-2 is implicated in various adhesive interactions of monocytes, macrophages and granulocyte as well as in mediating the uptake of complement-coated particl It is identical with CR-3, the receptor for the iG3b fragment the third complement component. It probably recognizes the R-C-peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptide of fibrinogen gamma chain.
                                                                                                                                                                                                                                                                                                      3D-STRUCTURE MODELING OF 17-616.
MEDLINE=98226734; PubMed=9560195;
Oxvig C., Springer T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.B. Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.; "Cation binding to the integrin CD11b I domain and activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 148-337.

MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;

MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;

MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;

MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;

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MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;

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MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;

MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;

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MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;

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MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;

MEDLINE=98362595; PubMed=98362595; DOI=10.1016/S0969-2126(98)00093-8;

MEDLINE=98362595; PubMed=98362595; DOI=10.1016/S0969-2126(98)00093-8;

MEDLINE=98362595; PubMed=98862595; DOI=10.1016/S0969-2126(98)00093-8;

MEDLINE=98362595; PubMed=98862595; DOI=10.1016/S0969-2126(98)00093-8;

MEDLINE=98362595; PubMed=98862595; DOI=10.1016/S0969-2126(98)00093-8;

MEDLINE=98362595; PubMed=98862595; PubMe
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MEDLINE=95171458; PubMed=7867070; DOI=10.1016/0092-8674(95)90517-0;
Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
"Crystal structure of the A domain from the alpha subunit of integr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87076671; PubMed=3539202; DOI=10.1016/0167-4838(86)90037-3; Pierce M.W., Remold-O'Donnell E., Todd R.F. III, Arnaout M.A.; "N-terminal sequence of human leukocyte glycoprotein Mo1: conservation across species and homology to platelet IIb/IIIa."; Biochim. Biophys. Acta 874:368-371(1986).
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MEDLINE=96363671; PubMed=8747460; DOL=10.016/80969-2126(01)00271-4;
Lee J.O., Banketon L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway fo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of the Blood 79:865-870(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pahl H.L., Rosmarin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmentally regulated Proc. Natl. Acad. Sci. U.S
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"The promoter of the CD11b gene directs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-9 FROM N.A. MEDLINE=92073318; PubMed=1683702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hickstein D.D.,
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Hickey M.J., Ozols
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S.A. 88:10525-10529(1991)
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                                                                                                                                                                                                                                                                                                                                  DOI=10.1073/pnas.95.9.4870;
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MIM; 120980; -.
GO; GO:0008305; C:integrin complex;
GO; GO:0007155; P:cell adhesion; TA:
InterPro; IPR000413; Integrin_alpha
InterPro; IPR002035; VWF_A.
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SIMILARITY: Contains 7 FG-GAP repeats.
SIMILARITY: Contains domain.
DATABASE: NAME=PROW; NOTE=CD guide CD11b entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd1lb.htm".
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DOMAIN: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Predominantly expressed in monocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-M
                                                                                                                  1BHO,
1BHQ,
1IDO,
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1A8X; Mc
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S52154; AAB24821.1;
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$52152; AAB24821.1;
                                                          HGNC: 6149;
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X-ray; A=137-331.
X-ray; A=144-337.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration - MBL outstation -
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RESULT 14
CA1C_HUMAN
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                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.

MEDLINE-97288521; PubMed-9143499; DOI=10.1006/geno.1997.4638;

AGERECKE D.R., Olson P.F., KROLI J.H.M., Taylor R.}

A Hudson D.L., Champliaud M.-F., Olsen B.R., Burgeson R.E.;

"Complete primary structure of two splice variants of collagen XII,
and assignment of alpha 1(XII) collagen (CCL12A1), alpha 1(X)

"collagen (CCL9A1), and alpha 1(XIX) collagen (CCL19A1) to human

"chromosome 6q12-q13.";

Genomics 41:336-242(1997).

"Genomics 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                099715; Q99716;
15-JUL-1998 (Rel. 36, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
25-OCT-2004 (Rel. 45, Last annotation
Collagen alpha 1(XII) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00092; VWA; 1
PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN
SWART; SW00191; Int alpha; 1
SWART; SW00327; VWA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium; Cell adhesion; Direct
                                                                                                                                                           <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Integrin; Magnesium; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA1C_HUMAN
                                                              ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=The final tissue form of collagen X
homotrimers of either isoform Long or isofo
combination of isoform Long and isoform Sho
                Name=Long;
IsoId=Q99715-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF01839;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGEKFGDPLGYEDVI PEADRE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTFKEFONNPNPRSLVKPITQLL--GRTHTATGIRKVVRELFNITNGARKNAFKILVVIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
1152
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                       Sequence=Displayed,
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Pred. No. 0.0
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                                                                 of collagen XII may contain
Long or isoform Short or an
nd isoform Short;
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: Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing;
Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                        any
                                                                                                                                                                                                                                                                                                                                                                                                      XII,
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Genew; HGNC:2188; COL12A1.

MIM; 120320; -.

GO; GO:0005595; C:collagen type XII; TAS.
GO; GO:0005501; P:skeletal development; TAS.
InterPro; IPRO03160; Collagen.
InterPro; IPRO03961; FN III.
InterPro; IPRO03961; FN III.
InterPro; IPRO03961; FN III.
InterPro; IPRO03961; FN III.
InterPro; IPRO03961; WFA.
Pfam; PF01391; Collagen; 4.
Pfam; PF01391; Collagen; 4.
Pfam; PF02210; TSP_N; 1.
Pfam; PF02210; TSP_N; 1.
Pfam; PF020092; VWA; 4.
PRINTS; PRO0453; VWFAADOWAIN.
  Hydroxylation; 1
SIGNAL 1
CHAIN 25
DOMAIN 25
DOMAIN 333
DOMAIN 631
DOMAIN 722
DOMAIN 904
DOMAIN 905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative splicing; Cell adhesion; Collagen; Direct protein sequencing; Extracellular matrix; Glycoprotein; Hydroxylation; Repeat; Signal; Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U73778; AAC51244.1; -.
EMBL; U73779; AAD40483.1; -.
HSSP; P18614; 1MHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50853; FN3; 18. PROSITE; PS50234; VWFA; 4.
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PTM: Prolines at the third position of the triunit (G-X-Y) are hydroxylated in some or all one of the triunit (G-X-Y) are hydroxylated in some or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or all one or a
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similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        short and long isoforms appear in amnion, chorion, skeletal muscle, small intestine, and in cell culture of dermal fibroblasts, keratinocytes and endothelial cells. Only the
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    813
9904
1086
1199
11384
11474
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11933
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422
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VWFA 1
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                                      Q8C6K9;
Q8C6K9;
01-MAR-2003
01-MAR-2003
01-JUN-2003
        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sunctation update)
01-JUN-2003 (TrEMBLrel. 24, Last sunctation update)
Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-
length enriched library, clone:E330019B14 product:hypothetical vor
Willebrand factor type A domain containing protein, full insert
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(Mouse)

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RP SEQUENCE PROM N.A.

2 STRAIN=C57BL/6J; TISSUE=Ovary;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hayashida K., Hayatsu N., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Okazaki Y.,

RA Kurihara C., Monora K., Numazaki R., Ohno M., Ohaato N., Okazaki Y.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohaato N., Okazaki Y.,

RA Salto R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

RA Sasaki D., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

RA Submiteed (JUL-201) to the EMBL/GenBank/DDBJ databases.

RMED, PATSAACE, STROMBORIA.
PRINTS; PROUDENT; TART; SM00327; Tesc0234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/63; TISSUE=Ovary;

MEDLINE=20530913, PubMed:11076861; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/60; TISSUE=Ovary;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new ge

Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Ovary;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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SEQUENCE FROM N.A.
STRAIN=(57BL/GJ; TISSUE=Ovary;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                 MGD; MGI:2444259; E330026B02Rik.
InterPro; IPR002035; VWF_A.
Pfam; PF00092; VWA; 6.
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Mammalia; Eutheria; Rodentia;
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Sciurognathi; Muridae; Murinae; Mus.
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Tang YT, Liu C, Asundi V, Chen R, Wang J, Wang Z, Wehrman T, Xu C, Zhou P, Goodrich R, Drmanac RT;

Xue Ŋ,ĸ

Qian XB, Yang Y,

Ren F, 1 Zhang J,

Wang D; , Zhao QA;

WPI; 2001-442253/47.

N-PSDB; AAI58132.

Novel nucleic acids and polypeptides, useful as central nervous system injuries.

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Example 4; SEQ ID NO 2121; 10078pp; English.

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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-005598042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-CCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
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(OKBE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
WPI; 2003-720708/68
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                                                         Rottman JB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial; gene therapy; von Willebrand factor A-like domain amino acid sequence; vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax; inhalation anthrax; human; TANGO197; his tag; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF.
                                                                                                             (ROTT/)
(OKEE/)
(OZKA/)
                                                                                                                                                                                                                       20-DEC-2001; 2001US-00038307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                               ) ROTTMAN J B.
) O'KEEFE T L.
) OZKAYNAK E.
) HEALEY J J.
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Best Local Similarity 100
Matches 181; Conservative
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                                                                                                                                                                                   Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis;
                                                                                                                                                                                                                                      TANGO, 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel diseases; septic shock; ulcerative colltis; crohn's disease; chronic myelogenous leukemia; cancer; liver diseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or amelilarating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWP.
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   30-DEC-1998;
                                   23-DEC-1999;
                                                                                                                                                                       prophylatic,
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                                                                                                                                     Homo sapiens
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DB; ADM64583.
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Pred. No. 2e-96;
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid sequences encoding TANGO-1 and 239 polypeptides useful for the treatment arthritis, psoriasis and autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                     Human anthrax toxin receptor
                                                                                                                                                                                                                                                                                                                                                                                                 08-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP54905;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host disease, rheumatoid arthritis, psoriasis, inflammatory bowel disease,
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                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                            Anthrax; toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP54905 standard; protein;
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                                                                                                                        Peptide
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                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                         receptor; human; antibacterial
                                                                                     /label= Signal_peptide
                                                                                                                                                 Location/Qualifiers
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Pred. No. 2e-96;
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asthma,
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ma, rheumatoid
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC as a human anthrax toxin receptor (ATR) polypeptide on the basis of CC identity to a newly isolated human ATR (see ABP54903). The 2 polypeptides CC are identical between amino acids 1-317, but differ thereafter at the C-CC terminus. The present polypeptide, encoded by IMAGE CLONE 4563020, has no CC previously known function, and there has been no prior indication that it C is a complete or partial ATR. The invention provides ATR polypeptides and CC polynucleotides, vectors, host cells, and transgenic and knock-out CC animals. It also provides methods for identifying molecules that bind the CC ATR and which reduce the toxicity of anthrax toxin. A claimed method for treating anthrax in a human or animal involves administering an agent CC treating anthrax in a human or animal involves administering an agent CC agents include the present polypeptide or a PA-binding fragment of it, a monoclonal or polyclonal antibody, a polysaccharide, a fusion protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 181; Conserv
   fusion; von Willebrand factor A-like domain; vWF;
                                  Human TANGO
                                                                   22-APR-2004
                                                                                                                                     ADI00534 standard; protein; 333 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated polypeptide useful for identifying agent that prevents or reduces effect of anthrax toxin on host cell, for treating human or non-human animal suffering from anthrax.
                                                                                                    ADI00534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 333 AA;
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                                  protein.
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100.0%; Pred. No. 2e-96;
tive 0; Mismatches
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 antibacterial;
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RESULT 7
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Best Local Similarity
antibacterial; over willebrand in the very serious version and the very serious versions and the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the version of the
                                                                                                              Human von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ROTT/) ROTTMAN J B.
(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-likedomain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF.
                                                                                                                                                                    03-JUN-2004
                                                                                                                                                                                                                             ADM64568;
                                                                                                                                                                                                                                                                                ADM64568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 333 AA;
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gene therapy;
factor A-like domain amino ;
sequence; anthrax; Bacillus
                                                                                                                                                                                                                                                                              protein; 333
                                                                                                                                                                  entry)
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100.0%; Pred. No. 2e-96;
tive 0; Mismatches
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  acid sequence;
s anthracis; cutaneous anthrax;
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Best Local Simi
Matches 181;
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                         Human TANGO 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 26; SEQ ID NO 2; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-likedomain (VWF) amino acid sequence and an amino acid sequence heterologous
                                                                    22-APR-2004
                                                                                                                                                      ADI00554 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 333
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OZKAYNAK E.
HEALEY J J.
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                      protein -
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Pred. No. 2e-96;
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                      plasmid p0613
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                                                                  03-JUN-2004 (first entry)
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(OKEE/)
(OZKA/)
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The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 FLAG fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor Adomain (VWF) amino acid sequence and an amino acid sequence heterological states of the comprise of the comprise of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the compression of the com
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) O'KEEFE T L.
) OZKAYNAK E.
) HEALEY J J.
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Pred. No. 2.1e-96;
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                    ADI00556
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                                                 ADI00556 standard; protein;
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(OKEE/)
(OZKA/)
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von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; human; TANGO197; FLAG; fusion protein; gene.
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100.0%; Pred. No. 2.1e-96;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                       New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (VWF) amino acid sequence and an amino acid sequence heterologous
                                                                                                                                                                                                                                             Sequence 345 AA;
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inhalation anthrax; human; TANGO197; his tag; fusion protein; gene.
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                                                                                                                                                                                                                  GFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLKMSFIVFSTRGTTLMKLTEDREQ
  EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSCI
                                                                                                                                                                                                                                                                                                                               Conservative
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sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
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                                                                                                                                                                                                                                                                                                                      Score 943; DB 7; L
Pred. No. 2.1e-96;
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                                                           Novel isolated polypeptide useful for identifying reduces effect of anthrax toxin on host cell, for
                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                            Region
                       Claim 1;
                                              human animal suffering from anthrax.
                                                                                                  N-PSDB; ABV73881.
                                                                                                              WPI; 2002-713235/77.
                                                                                                                                      Young JAT,
                                                                                                                                                                                         05-DEC-2000; 2000US-0251481P
                                                                                                                                                                                                               03-OCT-2001; 2001WO-US030941
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                                                                                                                                                                                                                                                                                                          Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anthrax; toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP54903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Кeу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human anthrax toxin receptor
                                                                                                                                                              (WISC ) WISCONSIN ALUMNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E 222
                      Page 29-30; 45pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                     Bradley KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "PA-binding fragment, begins at any amino acid
the range 27-43 and ends at any amino acid in the rang
221-321, region specifically described in Claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor; human; antibacterial.
                                                                                                                                                                                                                                                                                                                                            /note= "forms metal ic motif with amino acid
                                                                                                                                                                                                                                                                                                                                                                                    motif with
                                                                                                                                                                                                                                                                                                                                                                                                                          motif with
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "forms metal ion-dependent adhesion site (MIDAS)
motif with amino acid residues 50, 54, 118 and 150"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    motif with
                                                                                                                                                                                                                                                                                                                                                                                  /note= "forms metal ion-dependent adhesion
notif with amino acid residues 50, 52, 54 a
                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "forms metal ion-dependent
motif with amino acid residues 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "forms metal ion-dependent adhesion
notif with amino acid residues 52, 54, 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "von Willebrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 368
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                                                                                                                                                                                                                                                                                           "cytoplasmic
                                                                                                                                                                                                                                                                                                                    "putative transmembrane
                                                                                                                                                               RES
                                                                                                                                      Collier RJ,
                      English
                                                                                                                                                               FOUND
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                                                                                                                                      Mogridge JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor A domain"
                                                                                                                                                                                                                                                                                                                      domain"
                                                           agent that prevents or treating human or non-
                                                                                                                                                                                                                                                                                                                                                                                                                       adhesion, 52, 118
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and 150"
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and 150"
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The

present sequence is the protein sequence of a human surface- bound

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RESULT 13
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ID ADM644586
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
  WPI; 2003-829643/77
N-PSDB; ADM64585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides ATR polypeptides and polynucleotides, vectors, host cells, and transgenic and knock-out animals. It also provides methods for identifying molecules that bind the ATR and which reduce the toxicity of anthrax toxin. A claimed method for treating anthrax in a human or animal involves administering an agent that inhibits binding between PA and ATR at a level effective to reduce the severity of anthrax. Suitable agents include ATR or a PA-binding fragment of ATR, a PA-binding polypeptide at least 80% identical to these, a fusion protein, a monoclonal or polyclonal antibody, a polysaccharide, a lipid or a
                                                                                  Rottman JB, O'keefe
                                                                                                                                                                        (OKEE/)
(OZKA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial;
von Willebrand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM64586;
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                                                                                                                                                                                                                                                                                     20-DEC-2001; 2001US-00038307
                                                                                                                                                                                                                                                                                                                                             20-DEC-2001; 2001US-00038307
                                                                                                                                                                                                                                                                                                                                                                                                        17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003134786-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; human; TANGO197; immunoglobulin G; IgG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANGO197 extracellular domain-mutant IgG Fc fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM64586 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 368
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                                                                                                                                                                                                                                (ROTT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42
                                                                                                                                    ) ROTTMAN J B.
) O'KEEFE T L.
) OZKAYNAK E.
) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy;
factor A-like domain amino acid sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 943; DB 5; 100.0%; Pred. No. 2.3e-96; ... Mismatches 0;
                                                                                     Ozkaynak E,
                                                                                     Healey JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 368;
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New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF.
                                                                                                                                                                 A-like
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Claim 44; SEQ ID NO 10; 64pp; English.

heterologous to the vWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a fusion protein comprising human TANGO197 extracellular region, minus the DG residues closest to the transmembrane region, and The invention factor A-like G237A. describes a fusion polypeptide comprising domain (vWF) amino acid sequence and an an Q (IgG) fragment of crystallisation (Fc) with mutations amino acid sequence a von Willebrand

Sequence 384 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene 4 encoded secreted protein HWLFR02, SEQ ID NO:94.
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Homo sapiens

Protein Peptide

> /label= Signal_peptide Location/Qualifiers

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"Mature human secreted

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CC Pathological conditions can be diagnosed by determining the amount of the constitutions can be diagnosed by determining the amount of the constitutions can be diagnosed by determining the amount of the constitutions in the new genes. Specific uses are described for each of the 28 genes, constitutions in the new genes. Specific uses are described for each of the 28 genes, constitutions on the tissues in which they are most highly expressed, and include constitutions of the inventorial actions in the new genes, specific disgraphic constitutions of proliferative constitutions of proliferative disorders, diseases of the immune system, AIDS, autoimmune consistent of proliferation, altergies, and include consistent of proliferation, altergies, consistent of sorders, and inchemetorial, asthma, skin disorders, altergies, consistent of sorders, and inchemetorial, asthma, skin disorders, and inchemetorial, asthma, skin disorders, and infections. The propagancy-related disorders, disorders, gastrointestinal disorders, consistent consistent and inchemetaxis, and cound healing and epithelial cell consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consistent consi
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30-JUN-2000; 2000US-0215133P
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions
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Matches 181; Conserv
                                                                                                                                                                                                                                                                                                                       The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. acquired haematopoietic disorders, meural disorders (e.g. Alzheimer's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Albumin fusion protein; therapeutic protein X; human albumin; HA human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
                                                                                                                                                                                                                                                                                    Sequence
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25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 874-875; 2102pp; English.
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                             IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS
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Search completed: June 13, 2005, 19:56:54 Job time : 68.0133 Becs	222 E 222	181 E 181	162 ERBANKSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI 221	121 EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI 180

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Result
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   GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Matches

53;

Conservative

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Mismatches

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Gaps

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Query Match Best Local Similarit	NESULT 1 US-08-286-899-37 US-08-286-899-37 Sequence 37, Application parent No. 5470953 GENERAL INFORMATION: APPLICANT: Gallatin, APPLICANT: Van der VITLE OP INVENTION: VAN DER CORRESPONDENCE ADDRESSE MATERION: UNITED CORRESSES: MATERION: UNITED CORRESSES: MATERION: UNITED COMPUTER READABLE FOR MEDIUM TYPE: Flopp COMPUTER READABLE FOR MEDIUM TYPE: Patentin CURRENT APPLICATION UNMBER: FILING DATE: SOFTWARE: PATENTIN NUMBER: FILING APPLICATION UNMBER: FILING DATE: CLASSIFICATION NUMBER: FILING DATE: 31-474-01 PRESENTATION NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REFRENCE/DOCKET NUMBER: REGRENCE/DOCKET NUMB		28 138.5 14 30 138.5 14 31 138.5 14 32 138.5 14 33 138.5 14 34 138.5 14 36 136.5 14 37 132.5 14 40 132.5 14 40 132.5 14 42 132.5 14 43 132.5 14 43 132.5 14 43 132.5 14 43 132.5 14 43 132.5 14 43 132.5 14
15.0%; Score 141.5; DB 1; rity 27.7%; Pred. No. 4.2e-07;	OB-286-889-37 OB-286-889-37 OBQUENCE 37, Application US/08286889 Patent No. 5470953 GENERAL INFORMATION: APPLICANT: Gallatin, W. Mich APPLICANT: Gallatin, W. Mich APPLICANT: Gallatin, W. Mich APPLICANT: Gallatin, W. Mich APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: ADDRESSE: MATERAIL, O'Toole, Gerstein, Murray STREET: 233 South Wacker Drive, 6300 Sear Tower CITY: Chicago STATE: Illinois COUNTRY: United States ZIP: 60606-6402 ZIP: 60606-6402 ZIP: 60706-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/286,889 FILLING DATE: 23-DEC-193 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: US/08/286,889 FILLING DATE: 23-DEC-193 ATTORNEY/AGENT INFORMATION: NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: P38,659 REFERENCE/DOCKET NUMBER: P38,659 REFERENCE/DOCKET NUMBER: P38,659 REFERENCE/DOCKET NUMBER: P38,659 REFERENCE/DOCKET NUMBER: P38,659 REFERENCE/DOCKET NUMBER: D312-474-6348 TELEFAX: 312-474-0448 TELEFAX: 312-474-0448 TELEFAX: 312-474-0448 TELEFAX: 312-474-0448 TELEFAX: 312-474-0448 TELEFAX: 312-474-0448 TELEFAX: 312-474-0448 TELEFAX: 312-474-0448 TELEFAX: 312-474-0448 TELEFAX: 312-474-0448 TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: mino acids TYPE: protein MOLECULE TYPE: protein	ALIGNMENTS	7 1161 1 US-08-362-652-53 7 1161 2 US-08-605-672-53 7 1161 2 US-08-402-293A-53 7 1161 2 US-08-943-363-53 7 1161 3 US-09-133-043-63 7 1161 4 US-09-688-307A-53 7 1161 4 US-09-580-259-53 7 1161 4 US-09-795-872-5 5 216 4 US-09-795-872-5 5 216 5 PCT-US95-04439-1 1 1152 6 5424399-2 1 1152 6 5424399-2 1 1153 1 US-08-286-889-3 1 1153 1 US-08-405-618-3 1 1153 1 US-08-405-618-3 1 1153 2 US-08-605-672-3
Length 1151;	grin Alpha Subunit Ver		Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 43, Appl Sequence 43, Appl Sequence 3, Appli Sequence 3, Appli

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                                                                             Matches
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PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/362,6
PILING DATE: 21-DEC-1994
ATTORNEY AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC DOS/MS-DOS
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LENGTH: 1151 amino aci
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SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                            TELEFAX: 3.
                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 233 Sc
CITY: Chicago
                                                                                                                                                                                                  TOPOLOGY:
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                                  3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                         h 15.0%; Score 141.5; DB 1; Length 1151; Similarity 27.7%; Pred. No. 4.2e-07; 53; Conservative 38; Mismatches 75; Indels 25;
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                                                                                                                                                                                                               amino acid
DIAPLIDGGGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTBFKNIL
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Best Local Similarity
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Patent No. 5766850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
TYPE: amino acid
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 0:
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312-474-0448
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116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA 166
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                                                                                                                                                                                                       15.0%; Score 141.5; DB 1; 27.7%; Pred. No. 4.2e-07; ative 38; Mismatches 75;
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RESULT 4
US-08-605-672-37
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                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32684
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APPLICANT: Gallat
APPLICANT: Van de
                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 312-474-6300
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TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
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                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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CLASSIFICATION: 530
                                                                                                                                                                                                                                                Local
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                                    116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 166
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                                                                          202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 256
                                                                                                                                                  142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
                                                                                                                                                                                        3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
                                                                                                              DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 115
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                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                            15.0%; Score 141.5; DB 2; 27.7%; Pred. No. 4.2e-07; tive 38; Mismatches 75;
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                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                Indels
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US-08-482-293A-37
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                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
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INFORMATION FOR SEQ ID NO:
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CITY: Chicago
Illinois
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
TOTAL OF SECUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS LENGTH: 1151 amino ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                        Local Similarity
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167
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                                                                          116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFFVNDGFQA 166
                                                                                                                                                                                          142 DIAPLIDGSGSINORDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
                                                                                                                                                  57 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 115
                                                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                              3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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LOGIIHSILKK 177
                                      PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
                                                                                                              DPOSLVDPIVQLQ-----GLTYTATGIRTVMEBLFHSKNGSRKSAKKILLVITDGQKYRD 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                          1151 amino acids
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                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                      15.0%; Score 141.5; DB 2
27.7%; Pred. No. 4.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version
                                                                                                                                                                                                                                                                                                          DB 2;
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US-08-943-363-37
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                                                                                                                                                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein -08-943-363-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTONNEY/AGENT INFORMATION:
NAME: WIlliams Jr., JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27.866/32684
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gallatin, W. MICNAEL
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOPTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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313
                                   167 LOGIIHSILKK 177
                                                                             257
                                                                                                                116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFFVNDGFQA 166
                                                                                                                                                          202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
                                                                                                                                                                                                                                       142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL
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XGY: linear
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LRSIQRQLQEK 323
                                                                               PLEYSDVI PAADKA ---
                                                                                                                                                                                                DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 115
                                                                                                                                                                                                                                                                             DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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LRSIQRQLQEK 323
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                                                                                                                                                                                                                                                                                                                     15.0%; Score 141.5; DB 2; larity 27.7%; Pred. No. 4.2e-07; Conservative 38; Mismatches 75;
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                                                                             -GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA
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; ORGANISM: Rattus rattus
US-09-193-043-37
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CURRENT APPLICATION NUMBER: US/09/193,043

CURRENT FILING DATE: 1998-11-16

EARLIER APPLICATION NUMBER: 08/173,497

EARLIER FILING DATE: 1993-12-23

EARLIER FILING DATE: 1994-08-05

EARLIER FILING DATE: 1994-08-05

EARLIER APPLICATION NUMBER: 08/362,652

EARLIER APPLICATION NUMBER: 08/362,652

EARLIER APPLICATION NUMBER: 08/363,363

EARLIER FILING DATE: 1997-10-03

NUMBER OF SEQ ID NOS: 114
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                                      PRIOR APPLICATION NUMBER: 08/605,672
PRIOR FILING DATE: 1996-02-22
PRIOR APPLICATION NUMBER: 08/173,497
PRIOR FILING DATE: 1993-12-23
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR APPLICATION NUMBER: 08/362,652
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37, Application US/09688307A Patent No. 6432404
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GENERAL INFORMATION:
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                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/193,043
PRIOR FILING DATE: 1998-11-16
                                                                                                                                                                                                                                                                                                    APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: NO. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395el Human 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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APPLICATION NUMBER: 08/943,363
                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 DPQSLVDPIVQLQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOGIIHSILKK 177
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                   1994-12-21
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27.7%;
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Pred. No. 4.2e-07;
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TITLE OF INVENTION: NO. 6620915e1 Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT APPLICATION NUMBER: US/09/350,259
CURRENT ETLING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1993-12-23
EARLIER FILING DATE: 1994-08-05
EARLIER APPLICATION NUMBER: 08/286,865
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/363,652
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER PILING DATE: 1997-10-03
NUMBER: 08/95 E0 114
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US-09-350-259-37
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
APPLICANT: Van der Vieren, Monica
SOFTWARE: PatentIn Ver. SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/09350259
Patent No. 6620915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.0%; Score 141.5; DB 4; Best Local Similarity 27.7%; Pred. No. 4.2e-07; Matches 53; Conservative 38; Mismatches 75;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 464
OTHER INFORMATION: Xaa = a
NAME/KEY: misc_feature
LOCATION: 486
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OTHER INFORMATION: Xaa = a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1118
OTHER INFORMATION: Xaa = any or unknown amino acid
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LOCATION: 1117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 256
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US-08-485-618-55
; Sequence 55, A
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; ORGANISM: Rattus rattus
US-09-350-259-37
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Best Local Similarity 27.7%; Pred. No. 4.2e-07;
Matches 53; Conservative 38; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PRILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: W1111ams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3279
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/485,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 233 SOUCH
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60606-6402
                                       TYPE: amino acid
                                                                                                                                                         TELEFAX:
                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFFVNDGFQA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                                 1161 amino acids
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233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                            312-474-0448
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                        linear
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; TYPE: amino a
; TOPOLOGY: lin
; MOLECULE TYPE:
US-08-362-652-55
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US-08-362-652-55
; Sequence 55, Ap
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  Best Loc
Matches
                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                         TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT TATORNEY/AGENT TATORNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MERAL INFORMATION: W. Michael APPLICANT: Gallatin, W. Michael APPLICANT: Van der Vieren, Monica TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSE: Marzhall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                               TELEPHONE: 312-1-0448
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States ZIP: 60606-6402
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                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 15.0%; Score 141.5; DB 1; Length 1161; Similarity 27.7%; Pred. No. 4.2e-07; 53; Conservative: 38; Mismatches 75; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                                                                                                                                                                                       1161 amino acids
     Conservative
                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                      312-474-6300
                                                                                                                                                                                                   acid
15.0%; Score 141.5; DB 1
27.7%; Pred. No. 4.2e-07;
tive 38; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 08/173,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 08/286,889
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                                                                                                                                                                                                                                                                                                                                                                                                                           27866/32391
                                                 DB 1;
                                                 Length 1161;
  Indels
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Gaps
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                                                                                                                                                                      US-08-605-672-55
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                                                       Matches
                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino aci
                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60606-6402
                                                                                    Similarity
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                                                       Conservative
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
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APPLICATION NUMBER: US 08/173,497
                                                                                                                                                                                                                                                                                                                                                                                   NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
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3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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233 South Wacker Drive, 6300 Sear Tower
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                                                              15.0%;
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                                          38; Mismatches
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                                                              Score 141.5; DB 2
Pred. No. 4.2e-07;
                                                                                  DB 2;
                                          75;
                                          Indels
                                                                              Length 1161;
                                          25;
                                        Gaps
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                                                                Matches
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                                                                                                Query Match
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ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun
ADDRESSEE: Marchall, O'Toole, G300 Sear Tower
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                 TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
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APPLICATION NUMBER: 1
FILING DATE: 5-AUG-1:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                    NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                    TELEPHONE: 312-474-63
TELEFAX: 312-474-0448
TELEX: 25-3856
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                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                  LENGTH:
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152
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Van der Vieren, Monica
VENTION: No. 5831029el Human 2 Integrin Alpha Subunit
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                                                                Conservative
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                                                                38;
                                                             Score 141.5; DB 2;
Pred. No. 4.2e-07;
8; Mismatches 75;
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                                                                Indels
                                                                                              Length 1161;
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                                                                         Matches
                                                                                             Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/173,497
FILING DATE: 23-DEC-1993
                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC comm
                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                   MOLECULE TYPE: protein
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                         Local Similarity
                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                   relephone:
                                                                                                                                                                                                                                                                                                                                                                            NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
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 152 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTBFKNIL 211
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                                    DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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5-AUG-1994
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                                                                        15.0%; Score 141.5; DB: 27.7%; Pred. No. 4.2e-07 ative 38; Mismatches 7
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57 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 115

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US-09-193-043-55

¡ Sequence 55, Application US/09193043
¡ Patent No. 6251395
¡ GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6251395e1 Human 2
FILE REFERENCE: 27866/35004
[ CURRENT APPLICATION NUMBER: US/09/193,043
[ CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER APPLICATION NUMBER: 08/173,497
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER FILING DATE: 1994-08-05
[ EARLIER FILING DATE: 1994-08-05
[ EARLIER FILING DATE: 1994-12-21
[ EARLIER PILING DATE: 1994-12-21
[ EARLIER PILING DATE: 1997-10-03
] NUMBER OF SEQ ID NOS: 114
[ SOFTWARE: Patentin Ver. 2.0
[ SEQ ID NOS 55
[ LENGTH: 1161
] TYPE: PRT
[ ORGANISM: Rattus rattus
] US-09-193-043-55
Search completed: June 13, 2005, 20:05:10 Job time : 18.6748 secs
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                                                                                                             167 LOGIIHSILKK 177
                                                                                                                                                 267 PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA
                                                                                                                                                                                  116 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 166
                                                                                                                                                                                                                          323 LRSÍQRQLQEK 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 preqirqgleelqkvlpcgptymhegferaseQiyyenrQgyrta-sviialtpgelhep 115
                                                                                                                                                                                                                                                                                                                                       3 DLYFILDKSGSV-LHHWNEIYYFYEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
                                                                         LRSIQRQLQEK 333
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No.
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Maximum
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B B
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published
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Copyright (c) 1993 - 2005 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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jin2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
jin2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
jin2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
jin2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
jin2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
jin2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
jin2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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jin2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
jin2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
jin2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
jin2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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               US-10-038-307-26

US-10-201-292-26

US-09-796-753-12

US-10-038-307-2

US-10-201-292-2

US-10-201-292-22

US-10-201-292-22

US-10-201-292-22

US-10-201-292-24

US-10-201-292-24

US-10-201-292-25
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US-10-201-292-28
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Sequence 26, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 22, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence
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-09-796-753-5	US-10-104-047-2639	-10-368-087-1	-10-201-292-	-10-038-307-	-09-796-753-5	-10-047-542-9	0-201-292-	-10-201-292-1	-10-201-292-1	-10-038-307-	-10-038-307-1	-10-038-307-1	-10-201-292-1	-10-038-307-1	-10-201-292-	-10-474-794-3	-10-474-794-1	-09-918-715-3	-09-918-715-1	-09-833-245-6	-10-474-794-	-10-474-794-1	08-765A-	-10-301-822-1	-10-201-292-2	-10-038-307-2	-09-918-715-23	-09-918-715-18	-201-292-1	-10-038-307-1	0-201-292-3	-10-201-292-3	0-201-292-3
equence 54, App	e 263	equence 16, App	equence 6, Appl	equence 6, Appl	equence 52, App	equence 99, App	equence 16, App	equence 14, App	equence 10, App	equence 16, App	e 14,	e 10,	e 12,	e 12,	e 30,	e 301,	e 194,	301,	194,	620,		187,	1823	199,	20,	e 20,	232,	187,	18,	1Ce 18,	equence 36,	e 34,	equence 32,

ALIGNMENTS

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APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Met

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT PILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 26

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 328

TYDE: DET
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US-10-38-307-26
; Sequence 26, Application US/10038307
; Publication No. US20030134786A1
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-307-26
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                                                                                                                                                                                                                                   Query Match 100.0%; Score 943; DB 14; Best Local Similarity 100.0%; Pred. No. 1.6e-90;
                                                                                                                                                                                                                 Matches
                                             102
121 EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSCI 180
                                                                                                                                                                                                                 181;
                                                                                     61
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                                                                                                                                                       1 GFDLYFILDKSGSVLHHWNBIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ 60
                                                                              IRQGLBELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS 120
                                                                                                                                GFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ 101
                                          IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS
                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                              DB 14;
                                                                                                                                                                                                                                                            Length 328;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                 0;
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                                          161
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CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR PILING DATE: 1998-10-30
PRIOR PILING DATE: 1998-12-30
PRIOR PILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR PILLING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/229,388
PRIOR PILLING DATE: 1999-02-26
PRIOR PILLING DATE: 1999-02-26
PRIOR PILLING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/25,388
PRIOR PILLING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: 09/25,388
PRIOR PILLING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/25,389
PRIOR APPLICATION NUMBER: 09/312,359
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US-09-796-753-12
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US-10-201-292-26
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US-10-201-292-26
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SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 328
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09796753 Publication No. US20030027998A1 GENERAL INFORMATION:
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Best Local :
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APPLICANT: Theresa L. O'KEEPE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                  APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES
FILE REFERENCE: 7853-227-999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 100.0%; Score 943; DB 14; Similarity 100.0%; Pred. No. 1.6e-90; 81; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IROGLEELOKVLPGGDTYMHEGFERASEQIYYENROGYRTASVIIALTDGELHEDLFFYS
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Sequence 2, Application US/10038307
Publication No. US20030134786A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN

RESULT 4 US-10-038-307-2

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; ORGANISM: Homo sapiens
US-09-796-753-12
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SEQ ID NO 12
LENGTH: 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 943; DB 10; Best Local Similarity 100.0%; Pred. No. 1.6e-90; Matches 181; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 2000-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
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DR FILING DATE: 1999-12-23
DR APPLICATION NUMBER: 09/4:
DR FILING DATE: 1999-12-29
DR APPLICATION NUMBER: 09/4:
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TYPE: PRT
ORGANISM: Homo sapiens
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US-10-038-307-2
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT APPLICATION SECONDAMENT FILING DATE: 2003-02-14
NUMBER OF SECONDAMENT SECONDAMENT FILING DATE: 2003-02-14
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Best Local Similarity 100.
Matches 181; Conservative
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Judith J. HEALEY
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
TYPE: DET
                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Publication No. US20030144193A1
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Publication No. US20030134786A1
                                          Matches
                                                                Query Match
Best Local Similarity
                                                                                                                                       ORGANISM: Homo sapiens -10-201-292-22
                                                                                                                                                                                                                                                                                                                                         APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
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                                             181;
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  1 GFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ 60
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GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKANNAK

APPLICANT: Engin OZKANNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-299

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 26

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 345

TYPE: PRT

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  US-10-201-292-24
; Sequence 24, Application US/10201292
; Publication No. US20030144193A1
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US-10-038-307-24
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GENERAL INFORMATION:
APPLICANT: James B. ROTTWAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OP INVENTION: Tango 197 and Tango 216 Compositions
FILE REFERENCE: 7853-253-99
FILE REFERENCE: 7853-253-99
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030134786A1
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CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
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, LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-24
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Best Local Similarity
Matches 181; Conserv
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Best Local Similarity
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; ORGANISM: Homo sapiens
US-10-201-292-32
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-292-28
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/201,292

CURRENT PILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 32

LENGTH. 470
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REPERENCE: 7653-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 28
                                                                                                                                                              Query Match 100.0%; Score 943; DB 14; Best Local Similarity 100.0%; Pred. No. 2.7e-90; Matches 181; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32, Application US/10201292
Publication No. US20030144193A1
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Best Local Similarity 100.
Matches 181, Conservative
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                       61 IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS
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                                                                                                      1 GPDLYFILDXSGSVLHHWNBIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ
                                                                               GPDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ
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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNA
APPLICANT: Engin OZKAYNA
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 504
TYPE: PAT
ORGANISM: Homo sapiens
US-10-201-292-34
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US-10-201-292-36
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; ORGANISM: Homo sapiens
US-10-201-292-36
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US-10-201-292-34
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                                                      NUMBER OF SEQ ID NOS: 36
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 529
                                                                                                                                                                                                                                                                                                         Sequence 36, Application US/10201292 Publication No. US20030144193A1 GENERAL INFORMATION:
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                                                                                                                                APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KESFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7863-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
                                         TYPE: PRT
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Pred. No. 2.9e-90;
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RESULT 15

US-10-038-307-18

i Sequence 18, Application US/10038307

publication No. US20030134786A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNA

APPLICANT: JUdith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION NUMBER: US/10/038,307

CURRENT APPLICATION UNMBER: US/10/038,307

CURRENT FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 551
Search completed: June 13, 2005, 20:36:52
Job time: 59.0354 secs
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; ORGANISM: Homo sapiens
US-10-038-307-18
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                                                                                                                          222 E 222
                                                                                            181 E 181
                                                                                                                                                                                        102 IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS
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                                                                                                                                                                                                        61 IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYS
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                                                                                                                                                                                        161
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Minimum
Maximum
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Perfect score:
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                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                     Scoring table:
                                Post-processing: Minimum Match 0%
                                                                                                                                                        Searched:
                                                                     88
                                                                   seq length: 0 seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                       June 13, 2005, 19:47:08 ; Search time 12.9858 Seconds
(without alignments)
1341.095 Million cell upda
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943
Maximum
Listing
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45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

Result	Score	108	Length	, B	3 !	ion
2 2 F	132.5	14.4	1153		RWHU1B	cell surface
w	12	13.6	3124	N	A40020	a
۵	127.5		712	N	A45638	immunodominant
CS.	125.5		1163	ш	RWHU1C	cell surface glyc
თ	124.5	13.2	1153	N	800551	leukocyte surface
7	116	12.3	3051	N	S42373	Ω
8	114.5		760	<u> </u>	C2MS	classical-compleme
v	113		1747	N	A45974	collagen alpha
10	113	12.0	1857	N	831212	
11	113		1888	N	S78476	
12	111.5		929	N	I51027	type XII col
13	110		2944	N	A54849	agen al
14	105.5		764	<u>س</u>	BBHU	-
15	•		1029	<u>, </u>	S21369	collagen alpha 2(V
16	103.5		567	N	T28797	hypothetical
17	100		460	N	T23087	hypothetical
18	99	10.5	698	N	B96958	dnaK protein
19	97.5		496	N	A37979	3
20	97.5	10.3	761	ب	BBMS	complement facto
21	•	10.2	493	N	A33809	
22	95.5	10.1	500	ຎ	866522	cartilage matrix
23	95.5	10.1	1179	N	A53213	0
24	95	•	917	N	809646	collagen alp
25	95	10.1	1018	μ.	CGHU2A	collagen alpha
26	94	•	741	N	T46488	hypothetical
27	94	•	3176	N	CGHU3A	collagen alpha 3(V
28	93.5	9.9	574	N		
29	۵				A46283	מהסדסזסדנת מ

ALIGNMENTS

antigen Em100 - I C;Species: Eimeri C;Date: 01-Dec-19

Bimeria maxima

;Species: Eimeria maxima ;Date: 01-Dec.1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

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A,Cross-references: UNIPROT:Q04588; GB:M99058; NID:g158890; PID:g158891
A;Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)
F;45-218/Domain: von Willebrand factor type A repeat homology <VWA2>
F;238-296/Domain: thrombospondin type 1 repeat homology <THR1>
F;309-371/Domain: thrombospondin type 1 repeat homology <THR2>
F;372-432/Domain: thrombospondin type 1 repeat homology <THR3>
F;433-433/Domain: thrombospondin type 1 repeat homology <THR4>
F;433-433/Domain: thrombospondin type 1 repeat homology <THR5>
F;494-556/Domain: thrombospondin type 1 repeat homology <THR6>
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R;Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G.
R;Pasamontes, L.; Hug, D.; Humbelin, M.; Weber, G.
Mol. Biochem. Parasitol. 57, 171-174, 1993
A;Title: Sequence of a major Eimeria maxima antigen homologous
A;Reference number: A48569; MUID:93149203; PMID:8426611
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A; Residues: 1-724 < PAS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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Best Local S
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218 WGGVSSQİNGİİKAAC 233
                                                         164 FOALQGIIHSILKKSC 179
                                                                                                                                                                                     116 LFFYSERE-----ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV-FP--VNDG 163
                                                                                                                                                                                                                                                  107 QNADLLAAAAKKLPYAAGSTYTHLGLAKA-EEILFSFQKGGRDNAPKMILVMTDGA----
                                                                                                                                                                                                                                                                                                        60 QIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHED 115
                                                                                                                                                                                                                                                                                                                                                                           47 DVMLVVDESGSIGTSNYGKVRSFISNFAGTMPLSPDDVRVGLVTFGTSAVTRWDLSDSRA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISP-QLRMSFIVFSTRGTTLMKLTEDRE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
53; Conserv
                                                                                                                         ----SSRRSQTLSAAEKLRNRGVIIVVLGVGTGVNSAECRSIAGCDTSDTVECPRYLQSN 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.4%; Score 136; DB ilarity 27.0%; Pred. No. 0.000 Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 136; DB 2; Length (2...)
Pred. No. 0.00074;
""amatches 79; Indels
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cell surface glycoprotein CD11b precursor [validated] - human
N;Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion
eukocyte integrin alpha chain; neutrophil adherence receptor alphaM chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

protein

RESULT RWHU1B

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Blood 79, 865-870, 1992
A;Title: Characterization of the myeloid-specific CD11b
A;Reference number: IS2567; MUID:92144986; PMID:1346576
A;Accession: IS2567
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                              A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-499,501-1153 <FLE>
A;Cross-references: GB:S52227; NID:g263047; PIDN:AAB24821.1;
A;Cross-references: GB:S52227; NID:g263047; PIDN:AAB24821.1;
A;Note: sequence extracted from NCBI backbone (NCBI):121963)
R;Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout
Blochim. Biophys. Acta 874, 368-371, 1986
A;Title: N-terminal sequence of human leukocyte glycoprotein
A;Reference number: A90664; MUID:87076671; PMID:3539202
A;Accession: A26091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, G.J. Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: cDNA sequence for the alpham subunit of the human neutrophil adherence A;Reference number: A32218; MUID:89098893; PMID:2563162
A;Accession: A32218
A;Accession: A32218
A;Molecule type: mRNA
A;Residues: 9-1153 <HIC>
A;Residues: 9-1153 <HIC>
A;Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A;Note: part of this sequence was confirmed by protein sequencing R;Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-9 <SHED:
A;Cross-references: GB.M76724; NID:g180018; PIDN:ANAS8410.1;
A;Cross-references: GB.M76724; NID:g180018; PIDN:ANAS8410.1;
A;Arnaout, M.A.; Remold-O'Donnell, E.; Pierce, M.W.; Harris,
Proc. Natl. Acad. Sci. U.S.A. 85, 2776-2780, 1988
A;Title: Molecular cloning of the alpha-subunit of human and
A;Reference number: A94193; MUID:88190151; PMID:2833753
A;Accession: A30892
                                                                                                                                                     A;Experimental source: granulocytes R;Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G. Blood 79, 865-870, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n during evolution.
A;Reference number: A46526; MUID:93123748; PMID:8419480
A;Accession: A46526
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J. Cell Biol. 106, 2153-2158, 1988
A;Title: Amino acid sequence of the alpha subunit of human leukocyte adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567 R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A. J. Biol. Chem. 263, 12403-12411, 1988
                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 17-31 < PIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P11215; GB:J03925; NID:g187284; PIDN:AAA59544.1; PID:g307148
A;Note: part of this sequence was confirmed by protein sequencing
R;Arnaout, M.A.; Guta, S.K.; Pierce, M.W.; Tenen, D.G.
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A; Residues: 1-11:
A; Cross-reference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 917-1042 < AR2>
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A; Residues: 1-499,501-965, 'P', 967-1153 < ARN >
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: GB:M18044
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                                                                                                               promoter
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P.; Tenen, I
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J. Cell Biol. 115, 209-221, 1991

J. Tell Biol. 115, 209-221, 1991

J. Title: The complete primary structure of type XII collagen shows a chimeric molecule wide nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site. A, Reference number: A40020; MUID:92011862; PMID:1918137

A, Reference number: RANA

A, Residues: 1-3124 < YAM>

A, Residues: 1-3124 < YAM>

A, Residues: 1-3124 < YAM>

A, Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:g222811

A, Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:g222811

A, Cordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.

J. Biol. Chem. 264, 19772-19778, 1989

A, Title: Type XII collagen. A large multidomain molecule with partial homology to type IX

A, Accession: A34485; MUID:90062079; PMID:2584192

A, Accession: A34485
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C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol
C;Keywords: alternative splicing; calcium; cell adhesion; glycoprotein; heterodimer; magn
F;17-116,Domain: signal sequence #status predicted <SIG>
F;17-1183/Product: cell surface glycoprotein CD11b #status experimental <MAT>
F;17-1108/Domain: extracellular #status predicted <EXT>
F;17-1108/Domain: von Willebrand factor type A repeat homology <VWA2>
F;465-473/Region: calcium/magnesium binding #status predicted
F;530-538/Region: calcium/magnesium binding #status predicted
F;530-601/Region: calcium/magnesium binding #status predicted
F;1109-1134/Domain: transmembrane #status predicted <INT>
F;186,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N,Alternate names: fibrochimerin C,Species: Gallus gallus (chicken) C,Date: 10-Sep-1999 #sequence revisior C,Accession: A40020, A34485; B34485; Z,Accession: M, Yamada, K.M.; Yamada, K.M.; Yamada, K.M.; Yamada, K.M.; Yamada, K.M.; Yamada, K.M.; Yamada, K.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Y.M.; Yamada, Ya
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A;Cross-references: GB:M84477; NID:g180184;
C;Comment: A common beta chain (CD18) forms
C;Genetics:
C;Gene: GDB:ITGAM; CR3A
A;Cross-references: GDB:120599; OMIM:120980
A;Map position: 16p11.2-16p11.2
                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN.AAA48635.1; PID:g2
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                                                                                                     A; Molecule type: protein
A; Residues: 2772-2792; 2846-2873 < GOR2>
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                                               R;Gordon,
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
sion: A40020; A34485; B34485; A28037; S23814; S22254; S28811
ata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nish
M.K.; Gerecke, D.R.; Olsen, B.R.
1. Acad. Sci. U.S.A. 84, 6040-6044,
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Pred. No. 0.0026;
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matrix component

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A;Introns: 2845/3; 2863/3; 2867/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1
C;Keywords: alternative splicing; cell binding; coiled coil; connective tissue; disu
F;1-23/Domain: signal sequence #status predicted <SIG>
F;2-3/Domain: signal sequence #status predicted <SIG>
F;24,1189-3124/Product: collagen alpha 1(XII) chain #status predicted collagen form #status predicted <IIIA>
F;24,1189-3124/Product: collagen alpha 1(XII) chain short splice form #status predicted <IIIA>
F;24-114/Domain: IIIA #status predicted <IIIA>
F;337-301/Domain: von Willebrand factor type A repeat homology <VWA1>
F;337-301/Domain: iliB #status predicted <IIIB>
F;332-425/Domain: fibronectin type III repeat homology <VWA2>
F;629-1178/Domain: fibronectin type III repeat homology <FN3B>
F;629-1178/Domain: fibronectin type III repeat homology <FN3B>
F;629-1178/Domain: fibronectin type III repeat homology <FN3B>
F;12-895/Domain: fibronectin type III repeat homology <FN3B>
F;905-986/Domain: fibronectin type III repeat homology <FN3B>
F;197-1361/Domain: fibronectin type III repeat homology <FN3B>
F;198-1465/Domain: Fibronec
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A;Accession: A28037
A;Molecule type: mRNA
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A;Molecule type: mRNA
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1;
A;Cross-references: EMBL:M17375; NID:g211649; PIDN:AAA48718.1;
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A;Molecule type: mRNA
A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A;Cross-references: EMBL:X67327
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Trueb, J.; Trueb, B.
Blochim. Blophys. Acta 1171, 97-98, 1992
A;Title: The two splice variants of collagen XII share a A;Reference number: $28811; MUID:93042014; PMID:1420368
A;Accession: $28811
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A,Title: Type XII collagen is expressed in embryonic chick tendons. A,Reference number: S22254; MUID:88087065; PMID:3121603
A,Accession: S22254
A,Molecule type: protein
A,Residues: 2831-2832, T',2834, R',2836-2843;3002-3014 <DUB>
R,Trueb, J.; Trueb, B.
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A;Tit.De: A major oligomeric fibroblast proteoglycan identified A;Reference number: S23814; MUID:92362621; PMID:1323460
A;Recession: S23814
A;Molecule type: protein
A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',R;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',R;Dublet,B., van der Rest, M.
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                                                                                                                                                                                                                                                                                   F;2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>F;2946-3048/Domain: collagenous COL1 #status predicted <COL1>F;2946-3048/Domain: non-collagenous NC1 #status predicted <COL1>F;3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>F;3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>F;302,1006;1032;1044,1512;1767,2210,2273,2532,2683/Binding site:
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F;2028-2110/Domain:
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F,1756-1838/Domain:
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7,1474-1557/Domain: Fibronectin type III repeat homology FN3I>
7,1474-1557/Domain: Fibronectin type III repeat homology FN3I>
7,1655-1738/Domain: Fibronectin type III repeat homology FN3I>
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7,11756-1838/Domain: Fibronectin type III repeat homology FN3I>
7,11756-1838/Domain: Fibronectin type III repeat homology FN3I>
7,11756-1838/Domain: Fibronectin type III repeat homology FN3I>
7,1175-119/Domain: Fibronectin type III repeat homology FN3I>
7,2028-2110/Domain: Fibronectin type III repeat homology FN3IP-7,2119-2199/Domain: Fibronectin type III repeat homology FN3IP-7,21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2438-2440/Region: cell adhesion #status predicted
.2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status predicted
.2751-2992/Domain: collagenous COL2 #status predicted <COL2>
.2899-2901/Region: cell attachment (R-G-D) motif
                                       Query Match
Best Local Similarity
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                                       13.6%;
26.3%;
                                       Score 128; DB 2;
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N;Alternate names: leukocyte adhesion receptor p150,95 alpha chain C;Species: Homo sapiens (man) C;Species: Homo sapiens of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
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R;Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J. Mol. Biochem. Parasitol. 49, 277-288, 1991
A;Title: Sequence of the gene encoding an immunodominant microneme A;Reference number: A45638; MUID:92131064; PMID:1775171
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A45638
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A; Residues: 1-712 < TOM>
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216 SNWSNVTQQVNGIIKAAC 233
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                                                                                                                                                                                                    KVRWNLSDPKATNPSLAISAARSLSYSTGVTYTHYGLQDA-KKLLYDTNAGARNNVPKLV 157
                                                                                                                                                                                                                                                      QIRQGLEELQKVLPG------GDTYMHEGFERASEQIYYENRQGYR--TASVI 104
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                                                                                                                                                                                                                                                                                                        DVMLVVDESGSIGTSNFRKVRQFIEDFVNSMPISPEDVRVGLITFAT------RS 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 127.5;
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I backbone (NCBIN:77752, NCBIP:77756)
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rotein CD11c precursor -leukocyte adhesion recept

human

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C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on C;Genetics:
A;Gene: GDB:ITGAX; CD11C
A;Gene: GDB:ITGAX; CD11C
A;Gene: GDB:ITGAX; CD11C
C;Genetics:
C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat he C;Superfamily: cell surface glycoprotein; heterodimer; magnesium; tandem repei C;Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem repei P;1-19/Domain: signal sequence #status predicted <SIG>F;10-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>F;20-1163/Product: cell surface glycoprotein CD11c #status predicted <MAT>F;10-1107/Domain: von Willebrand factor type A repeat hemology <VWA4>F;1108-1133/Domain: transmembrane #status predicted <TNM>F;1134-1163/Domain: intracellular #status predicted <TNM>F;1134-1163/Domain: intracellular #status predicted <TNM>F;1134-1163/Domain: intracellular #status predicted <TNM>F;1134-1163/Domain: blycoprotein carbohydrate (Asn) (covalent) #status predicted <TNM>F;1134-1163/Domain: blycoprotein factor type A repeat hemology <VWA4>F;1134-1163/Domain: blycoprotein factor type A repeat hem
                                                                                                                                         leukocyte surface glycoprotein Mac-1 alpha chain precursor - N;Alternate names: complement-3 receptor alpha chain C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1991 #text_chan C;Accession: S00551; I59078 R;Pytela, R. R. Pytela, R. Pytela, R.
A; Molecule
                          A;Title: Amino acid sequence A;Reference number: S00551; A;Accession: S00551
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A;Residues: 1-755,'L','757-1163 <CO3>
A;Residues: 1-755,'L','757-1163 <CO3>
A;Cross-references: GB:M81695; EMBL:Y00093; NID:g487829; PIDN:AAA59180.1; PID:g487830
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: A common beta chain (CD18) forms a heterodimer with CD11b to form Mac-1 on
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J. Biol. Chem. 265, 2782-2788, 1990
A;Title: Genomic structure of an integrin alpha subunit,
A;Reference number: A35543; MUID:90153906; PMID:2303426
A;Accession: A35543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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A; Residues: 1-834 <CO2>
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A;Cross-references: UNIPROT:P20702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE--
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                                                             e of the murine MUID:88312584;
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PMID:3044779
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mer with CD11b to form Mac-1 on my
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A;Introns: 96/1; 166/3; 201/2, 201/2, 201/2, Eype F;512-679/Domain: von Willebrand factor type F;754-793/Domain: fibronectin type II repeat F;1201-1244/Domain: EGF homology <EGF>
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S42373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T20G5.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #t
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A;Residues: 1-1153 <PYT>
A;Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983 A;Cross-references: UNIPROT:P05555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983 A;Note: the authors translated the codon CAC for residue 569 as Gln
A;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83; 5644-5648, 1986
A;Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept A;Reference number: I59078; MUID:86287312; PMID:2942940
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A; Residues: 11-44 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-3051 <SMI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 VNDGFQALQGIIHSILKK 177
                                                                                                                                                                                                                                                                                                                                                    96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;
                                                                                                                                      3 DLYFILDKSGSVLHH--WNEIYYFVEQLAHKFI--SPQLRMSFIVFSTRGTTLMKLTE--
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                                            DREQIRQGLEELQKVLPG----GDTYMH---EGFERASEQIYYENRQGYR-----TASVI 104
DRDSLLKGISETQ-YLTGLTRTGAAIQHMVQEGF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V-DNFEALNTIQUOLQEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED--
                                                                                          DLVFLIDGSGSIGSYVFKNEVLRFVREFVELFEIGRSKTRVGLIQYSDQIRHEFDLDQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKD-FNETQLARIAD-----SKDHVFP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IHFTFNDFKRNPSPRSHVSPIKQLNGRTKTASGIRKVVRELFHKTNGARENAAKILVVIT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----REQIRQGLEELQKVLP----GGDTYMHEGFERASEQIYYE-NRQGYRTASVIIALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIVFLIDGSGSI----INIDF---QKMKEFVSTVMEQFKKSKTLFS-----LMQYSDEFR 197
                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: Z30423; NID: g458479; PID: g458485
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                                                                                                                                                                                                             28.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 124.5; DB Pred. No. 0.013;
                                                                                                                                                                                                             Score 116;
Pred. No. 0.
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                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GVIRYVIGVGNAFNKPQSRRELDTIASKPAGEHVFQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-Nov-1995 #text_change 09-May-2004
                                                                                                                                                                                                                                                                                                      A repeat homology <VWA1>
homology <2F1>
                                                                                                                                                                                                                                    DB
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                                                                                                                                                                                       74;
                                                                                                                                                                                                                                 Length 3051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                          573
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A;Pathway: complement classical pathway
C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; v
C;Superfamily: complement B/C2; complement factor H repeat homology; duplication; glycoprotei
F;1-18/Domain: signal sequence #status predicted <SIG>
F;1-250/Product: complement C2b fragment #status predicted <C2B>
F;22-89/Domain: complement factor H repeat homology <FH1>
F;94-149/Domain: complement factor H repeat homology <FH2>
F;156-210/Domain: complement factor H repeat homology <FH3>
F;151-760/Product: complement C2a fragment short form #status predicted <C2A>
F;251-605,613-760/Product: complement C2a fragment short form #status predicted <C2S>
F;259-449/Domain: von Willebrand factor type A repeat homology <VFA>
F;259-449/Domain: von Willebrand factor type A repeat homology <VFA>
F;478-747/Domain: trypsin homology #status atypical <TRY>
F;279-449/Domain: trypsin homology #status atypical <TRY>
F;27-62,9-89,94-116,122-10,470-500,499-515,593-609,647-674,685-715/Dis
F;27,117,297,340,474,478,663/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;514,570,689/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A/Status preliminary; translated from GB/EMBL/DDBJ
A/Status preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Roliduos: 660-677,'R', 679,681-723,'G',725 <RES>
A/Cross-references: GB:M16271; NID:g199289; FIDN:AAA39562.1; PID:g199290
C/Genetics:
A/Introns: 16/1; 91/1; 153/1; 212/1; 245/3; 290/3; 337/1; 384/1; 414/1; 461/1; 492/3; 53
C/Complex: The proenzyme forms a complex with C4a and is activated by cleavage into C2a, C/Function:
C/Function:
A/Description: cleaves complement C3 and complement C5 alpha chains
A/Pathway: complement classical pathway
C/Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; v
C/Keywords: alternative splicing; complement classical pathway; duplication; glycoprotei
F1-18/Domain: signal sequence #status predicted <SIG
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J. Biol. Chem. 265, 19040-19046, 1990
A;Title: Murine complement C2 and factor B genomic and cDNA cloning reveals different me A;Reference number: A36593; MUID:91035430; PMID:2229060
A;Accession: B36593
A;Molecule type: mRNA
A;Residues: 1-760 <ISH>
A;Residues: 1-760 <ISH>
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A;Cross-references: EMBL:M57891; NID:g192436; PIDN:AAA63294.1; DID:g192437
A;Falus, A.; Wakeland, E.K.; McConnell, T.J.; Gitlin, J.; Whitehead, A.S.; Colten, H.R. Immunogenetics 25, 290-298, 1987
A;Title: DNA polymorphism of MHC III genes in inbred and wild mouse strains.
A;Reference number: I54429; MUID:87192938; PMID:2883115
A;Recession: I54429
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 C;Accession: A38876; B36593; T54429
R;Ishikawa, N.; Monaka, M.; Wetsel, R.A.; Colten, H.R. submitted to GenBank, January 1991
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A;Accession: A38876
A;Molecule type: DNA
A;Residues: 1-760 <182>
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Best Local S
Matches 52
                                                                                                                                                                 261 NLYLLLDASQSVTEKDFDIFKKSAELMVERIFSFEVNVTVAIITFASQPKTIMSILSERS
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                                                                          60 QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYE------NRQGYRTAS----
                                                                                                                                                                                                                                           3 DLYFILDKSGSVLHHWNEIY-YFVEQLAHKFISPQLR--MSFIVFSTRGTTLMKLTEDRE 59
                                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                                                                         Similarity
Q-----DVTEVITSLDSASYKDHENATGANTYEVLIRVYSMMQTQMDRLGMETSAWKEI
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                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                             12.1%; Score 114.5; DB 1;
24.3%; Pred. No. 0.056;
41. Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 760;
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                                                                                                                                                                                                                                                                                                                                  49;
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374
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DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E

56

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A;Molecule type: protein
A;Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
A;Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime: F;40-204/Domain: von Willebrand factor type A respeat homology <VWA1>
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F;507-594/Domain: fibronectin type III repeat homology <FN3E>
F;607-594/Domain: fibronectin type III repeat homology <FN3E>
F;1625-707/Domain: fibronectin type III repeat homology <FN3E>
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F;1511-153/Domain: non-collagenous NC4 #status predicted <NC4>
F;1511-153/Domain: non-collagenous NC4 #status predicted <NC4>
F;15
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A;Cross-references: UNIPROT:P32018
A;Experimental source: embryo skin
A;Experimental source: setting the nucleotide translation
A;Note: sequence inconsistent with the nucleotide translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU>
R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne,
Eur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens
A;Reference number: S17035; MUID:92037585; PMID:1935930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Trueb, J.; Trueb, B.
Eur. J. Biochem. 207, 549-557, 1992
Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
A;Accession: S22916
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A;Reference number: S30085
A;Accession: S30085
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C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974; S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Canc
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Canc
J. Biol. Chem. 268, 12177-12184, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1472-1659 <GOR1>
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C;Species: Gallus gallus (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(XIV) chain precursor,
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                                             Query Match
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                                             Similarity
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                                             12.0%;
                                             Score 113; DB 2;
Pred. No. 0.2;
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                                                                                           Length 1747;
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     Indels
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Gaps
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R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Blochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: 331211; MUID:93185668; PMID:8444186
A;Accession: S31212
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1857 <MAEP
A;Roces-references: EMBL:X70792; NID:9288874; PIDN:CAA50063.1; PID:9288875
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Genetics:
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C;Date: 11-Mar-1998:
C;Accession: S31212
R;Waelchli, C:; True
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C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime F;1-28/Domain: signal sequence #status predicted <SIG> F;29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted <MAT> F;29-110/Domain: fibronectin type III repeat homology <FN3A> F;29-110/Domain: fibronectin type III repeat homology <FN3C> F;352-433/Domain: fibronectin type III repeat homology <FN3D> F;442-525/Domain: fibronectin type III repeat homology <FN3D> F;423-707/Domain: fibronectin type III repeat homology <FN3E> F;334-614/Domain: fibronectin type III repeat homology <FN3E> F;341-823/Domain: fibronectin type III repeat homology <FN3E> F;741-823/Domain: fibronectin type III repeat homology <FN3E> F;332-914/Domain: fibronectin type III repeat homology <FN3E> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> F;332-914/Domain: fibronectin type III repeat homology <FN3B> FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B- FN3B
collagen alpha 1(XIV) chain precursor,
C;Species: Gallus gallus (chicken)
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C;Species: Gallus gallus (chicken)
C;Date: 11-Mar_1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
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26.1%; Pred. No. 0.22;
tive 39; Mismatches 80; Indels 2
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A;Cross-references: UNIPROT:Q91145; EMBL:U19494; NID:g632647; PIDN:AAA80217.1; PID:g63264
F;155-236/Domain: fibronectin type III repeat homology <3FR>
F;631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
                                                                                                                                                                                                           A;Title: Monoclonal antibody MT2 identifies the urodele alpha A;Reference number: I51027; MUID:95246925; PMID:7729585 A;Accession: I51027
                                                                                                                                                                                                                                                                                                                                                                                                               type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime: F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-188/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <PN3A>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
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A;Residues: 1-416;1460-1811,1843-1888
A;Cross-references: EMBL:X70793
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A;Residues: 1-1888 <TRU>
A;Cross-references: UNIPROT:p32018; EMBL:X70793; NID:g288872; PIDN:CAA50064.1; PID:g28887
R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
                                                                                                         A; Molecule type: mRNA
A; Residues: 1-929 <WEI>
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A;Reference number: S78476
                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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Accession: 878476; 831211
                                                                                                                                                                                                                                                                                                                        i, Y.; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
Biol. 168, 503-513, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1213 DELITFVC 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1102 TKETLLEAIQQI--AYKGGNTKTGKAIKHARE-VLFTGEAGMRKGIPKVLVVITDGRSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1042 DLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTEFKLNAYK 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA--SVIIALTDGELHE 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DV-----NKVSREMQLDGFSFFAIGVADADYSELVNIGSKPSERHVFFVDD-FDAFTKIE 1212
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                                                                                                                                                                                                                                                                                       1 chain of type XII collage
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J. Invest. Dermatol. 99, 691-696, 1992
A;Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion A;Reference number: 156328; MUID:93107742; pMID:1469284
A;Accession: 156328
A;Accession: 156328
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Gelide type: mRNA
A;Residues: 'EFR',372-517,'DV',520-540,'W',542-1255 <RES>
A;Cross-references: GB:S51236; NID:g282308; PIDN.AAB24637.1; PID:g262309
A;Cross-references: GB:S51236; NID:g282308; PIDN.AAB24637.1; PID:g262309
A;Geltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, J. Biol. Chem. 264, 3822-3826, 1989
A;Hoference number: A30296; MUID:89139437; PMID:2537292
A;Accession: A30296; MUID:89139437; PMID:2537292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A;Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the A;Reference number: S16316; MUID:91334380; PMID:1871109
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A;Residues: 1-2944 <CHR>
A;Residues: 1-2944 <CHR>
A;Cross-references: UNIPROT:Q02388; GB:L02870; NID:g987124; PIDN:AAA75438.1; PID:g987125
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A;Title: Cloning of human type VII collagen. Complete primary sequence of t. A;Reference number: A54849; MUID:94327588; PMID:8051117
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A54849
A;Molecule type: protein
A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;
A;Note: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 'EFR',340-475,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,'C'A;Cross-references: DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:BAA02853.1; PID:g453699; A;Experimental source: keratinocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S. Biochem. Biophys. Res. Commun. 183, 958-963, 1992 A;Title: Molecular cloning and characterization of type A;Reference number: PH0844, MUID:9231902; PMID:1567409 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accession: PH0844 A;Accessio
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,Residues: 815-892,'E',894-1439 <PAR>
,Cross-references: GB:M65158, GB:S49017, NID:g180914, PIDN:AAA96439.1; PID:g180915
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Best Local Similarity
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Pred. No. 0.13;
7; Mismatches
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Best Local :
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F;2784-2944/Domain: cerl attachment (R-G-D) motif
F;2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BP
F;337,786,1109/Binding site: carbohydrate (Asn) (covalent) #status predic
F;2167,2176,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pr
F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experiment
F;2634,2802,2804/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;231-318/Domain: fibronectin type III repeat homology <FN1>
F;327-413/Domain: fibronectin type III repeat homology <FN2>
F;414-502/Domain: fibronectin type III repeat homology <FN3>
F;414-502/Domain: fibronectin type III repeat homology <FN3>
F;508-593/Domain: fibronectin type III repeat homology <FN4>
F;508-683/Domain: fibronectin type III repeat homology <FN5>
F;686-771/Domain: fibronectin type III repeat homology <FN7>
F;776-862/Domain: fibronectin type III repeat homology <FN7>
F;864-952/Domain: fibronectin type III repeat homology <FN8>
F;954-1045/Domain: fibronectin type III repeat homology <FN9>
F;1052-1219/Domain: von Willabrand factor type A repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1170-1172/Region: cell attachment (R-G-D)
F;1189-1253/Region: cysteine/proline-rich
F;1254-2783/Region: interrupted helical
F;1334-1336/Region: cell attachment (R-G-D)
F;2008-2010/Region: cell attachment (R-G-D)
F;2553-2555/Region: cell attachment (R-G-D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: coiled coil; extracellular matrix; glycoprotein; F;1-16/Domain: signal sequence #status predicted <SIG> F;17-2944/Product: collagen alpha 1(VII) chain #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 3p21.3-3p21.3
A;Note: defects in this gene can result in dominant and recessive A;Note: there are 118 introns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Greenspan, D.S.
Genet. 2, 273-278, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ر; Function: A; Description: Structural component of extracellular polymer associated with anchoring مرااها مدااه و A; Description: hydroxylysine; hydroxyprol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Complex: type VII collagen is probably a homotrimer
C;Function:
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A;Cross-references: GDB:128750; OMIM:120120
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173 SILKKSC 179
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                                                                                                                             DLFFYSEREANRSRDLGAIVYCVGVKDFNETQLARIAD -- SKDHVFPVNDGFQALQGIIH 172
                                                                                                                                                                                                                                   DLV---DTAAORLKGOGVKLFAVGIKNADPEELKRVASOPTSDFFFFVND-FSILRTLLP
                                                                                                                                                                                          GSGGDVIR-AIRELS--YKGGNTRTGAAILHVADHVFLPQLARPGVPKVCILITDGK-SQ 153
                                                                                                                                                                                                                                                                                                                       DIVFLLDGSSSIGRSNFREVRSFLEGLVLPFSGAASAQGVRFATVQYSDDPRTEFGLDAL
                                                                                                                                                                                                                                                                                                                                                                                        DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF---ISPQ-LRMSFIVFSTRGTT---LMKL
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Pred: No. 0.69;
7; Mismatches 83
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LVSRRVC

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A;Crobb-references: GB.J00185; GB.J00186

A;Note: the authors translated the codon TAC at 519 as Thr; the I R;Mole, J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.E.

J. Biol. Chem. 259, 3407-3412, 1984

A;Title: Complete primary structure for the zymogen of human complete primary structure for the zymogen of human complete primary structure for the zymogen of human complete primary structure for the zymogen of human complete primary structure for the zymogen of human complete response in A20751; MUID:84161997; PMID:6546754

A;Accession: A00934

A;Molecule type: protein; mRNA

A;Residues: 26-764 MOLD-

A;Crobs-references: GB.K01566

A;Note: nucleic acid translation differs from the sequence shown A;Note: 736-Ser was also found

A;Note: glycosylation sites were determined
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A;Title: The principal site of
A;Reference number: S14339; MU
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A;Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
R;Wu, L.; Morley, B.J.; Campbell, R.D.
Cell 48, 331-342, 1987
A;Title: Cell-specific expression of the human complement protein factor B gene: evidence number: A25971; MUID:87102880; PMID:3643061
A;Accession: B25971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 260-296,'T',298-764 <CHR>
A;Residues: 260-296,'T',298-764 <CHR>
R;Campbell, R.D.; Porter, R.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983
Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983
A;Title: Molecular cloning and characterization of the gene coding for human complement
A;Reference number: A19947; MUID:83273641; PMID:6308626
A;Accession: A19947
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Blochem. J. 209, 61-70, 1983
A;Title: Amino acid sequence of the Bb fragment from complement factor B. Sequence of A;Reference number: A19188; MUID:83204002; PMID:6342610
A;Contents: the final paper in a series documenting the sequence, glycosylation site, A;Accession: A19188
                                         A; Molecule type: protein
A; Residues: 270-329 <NIE>
                                                                                                                                                       A; Accession: S14339
                                                                                                                                                                                                                                                                                                                                              R; Niemann, M.A.; Bhown, A.S.; Miller,
                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M15082; NID:g187699; PIDN:AAA59625.1;
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A; Residues: 1-99 < WUL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:J00125
A;Accession: B19947
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A; Residues: 346-764 < CAM>
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A; Residues: 467-546; 550-595; 752-764 < WOO>
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site for carbohydrate
                                                                                                                                                                                                      of glycation of human MUID:91174758; PMID:20
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lysine
                                                                                                                                                                                      r numan complement
PMID:2006911
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under artificial conditions
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                                                                                                                                                                                                                                                                                                                                                                                                  PID:g553534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement factor
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F;1-25/Domain: signal sequence #status predicted <SIG's
F;26-764/Product: complement factor B #status experimental <MAT's
F;26-259/Product: complement factor B fragment #status experimental <BAF's
F;37-98/Domain: complement factor H repeat homology <FH1's
F;103-158/Domain: complement factor H repeat homology <FH2's
F;165-218/Domain: complement factor H repeat homology <FH2's
F;165-218/Domain: complement factor H repeat homology <FH3's
F;260-764/Product: C3/C5 convertase Bb fragment #status experimental <BBF's
F;268-458/Domain: von Willebrand factor type A repeat homology <VFA's
F;368-458/Domain: trypsin homology #status atypical <TRY's
F;37-76,62-98,103-145,131-158,165-205,191-218,778-596,551-527,599-615,656-682,695-725/Dig
F;122,142,285,378/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;259-260/Cleavage site: Arg-Lys (complement factor D) #status experimental
F;526,576,699/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 6p21.3-6p21.3

A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; 697.

A;Note: the list of introns may be incomplete
A;Note: gene is located in the major histocompatibility complex, class III region
C;Complex: complement factor B initially forms an inactive complex with complement factor
ment factor C3b forming active C3/C5 convertase; Ba is released
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-31, 'Q', 33-764 < RE2>
A; Cross-references: GB:L15702; NID:g291921;
C; Comment: 292-Cys has a free sulfhydryl.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Pathway: complement alternate pathway
C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; vc
C;Keywords: acute phase; complement alternate pathway; duplication; glycoprotein; hydrola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:BF
A;Cross-references: GDB:119726; OMIM:138470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: I57824
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic A;Reference number: I57824; MUID:94067177; PMID:8247029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; PID:g4261689 R;Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, S.; Volanakis, Mol. Immunol. 30, 1587-1592, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Human complement factor B: functional properties A; Reference number: I54409; MUID:94041399; PMID:8225386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 16-225,'F',227-259 <MOR>R;Schwaeble, W.; Luttig, B.; Sokolow
Immunobiology 188, 221-232, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: Bb is a serine proteinase; C3/C5 convertase cleaves complement C3 alpha
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A; Residues: 1-764 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Internal homologies of the Ba fragment from human complement component factor B, A;Reference number: A44628; MUID:84158524; PMID:6323161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Morley, B.J.; Can
EMBO J. 3, 153-157,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
   147
                                                                                                                                                102
                                                                                                                                                                                                                        328 DSSNADWVTKQLNEINYEDHKLKSGTNT-----KKALQAVYSMMSWPDDVPPEGWNRTR 381
                                                                                                                                                                                                                                                                                                                                                                     270 NIÝLVĽÚGSDŠIGASNFTGAKKCLVNLIÉKVÁSYGVKÞ--RYGLVTYATYPKIWVKVSEA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                         3 DLYFILDKSGSV-----LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                SVIIALTDG-
LARIADSKDHVFPVNDGFQALQGIIHSILKKS
                                                                        HVIILMTDGLHNMGGDPITVIDEIRDLLYIGKDRKNPREDYLDVYVFGVGPLVNQVNINA 441
                                                                                                                                                                                                                                                                                         --- DREQIRQGLEEL---- OKVLPGGDTYMHEGFERASEQIYYENR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 105.5; DI
Pred. No. 0.34;
                                                                                                                                            ELHEDLFFYSEREANRSRDLGAIVYCVG--VKDFNETQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN: AAA16820.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                             ---QGY-RTA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             56
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A, Molecule type: mRNA
A, Residues: 266-267, 'S', 269-294, 'L', 296-600 < CONS
A, Residues: 266-267, 'S', 269-294, 'L', 296-600 < CONS
A, Cross-references: GB:L06343; NID:g192671; PIDN:AAA37441.1; PID:g192672
A, Note: the sequence from Fig. 3 is inconsistent with that from Fig. 4 in having 306-Ile
C, Superfamily: collagen VI; von Willebrand factor type A repeat homology
C, Keywords: alternative splicing; cartilage; cell binding; connective tissue; disulfide
F, 12-28 Domain: signal sequence #status predicted < SIGS
F, 29-1029/Product: collagen alpha 2(VI) chain #status predicted < NATS
F, 29-265/Domain: globular #status predicted < NC2>
F, 29-265/Domain: collagenous #status predicted < NC2>
F, 376-378/Region: cell attachment (R-G-D) motif
F, 436-438/Region: cell attachment (R-G-D) motif
F, 499-501/Region: cell attachment (R-G-D) motif
F, 549-551/Region: cell attachment (R-G-D) motif
F, 549-551/Region: cell attachment (R-G-D) motif
F, 549-551/Region: cell attachment (R-G-D) motif
F, 623-799/Domain: yon Willebrand factor type A repeat homology < VWA2>
F, 621-1012/Domain: von Willebrand factor type A repeat homology < VWA3>
F, 841-1012/Domain: von Willebrand factor type A repeat homology < VWA3>
F, 841-1012/Domain: yon Willebrand factor type A repeat homology < VWA3>
F, 841-1012/Domain: yon Willebrand factor type A repeat homology < VWA3>
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c) Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C; Accession: S21369; S28808; S213745; S18863
R; Ibrahimi, X.Y.Z.; Bardon, X.Y.Z.; Dani, C.
submitted to the EMBL Data Library, April 1992
A; Reference number: S21369
A; Reference number: S21369
A; Reference number: S21369
A; Molecule type: mRNA
A; Residues: 1-1029 <IBR>
A; Cross-references: UNIPROT:Q02788; EMBL:X65582; NID:g49808; PIDN:CAA46541.1; PID:g49809
A; Cross-references: UNIPROT:Q02788; EMBL:X65582; NID:g49808; PIDN:CAA46541.1; PID:g49809
A; Cross-references: UNIPROT:Q02788; EMBL:X65582; NID:g49808; PIDN:CAA46541.1; PID:g49809
A; Title: Cloning of alpha2 chain of type VI collagen and expression during mouse develop A; Reference number: S28808; MUID:93143659; PMID:8380980
A; Molecule type: mRNA
A; Residues: 266-1029 <IB2>
A; Cross-references: EMBL:X62332; NID:g49906; PIDN:CAA44206.1; PID:g49907
A; Cross-references: EMBL:X62332; NID:g49906; PIDN:CAA44206.1; PID:g49907
A; Cross-references: EMBL:X62332; NID:g49906; PIDN:CAA44206.1; PID:g49907
A; Cross-references: EMBL:X62332; NID:g49906; PIDN:CAA44206.1; PID:g49907
A; Cross-references: EMBL:X62332; NID:g49906; PIDN:CAA44206.1; PID:g49907
A; Cross-references: EMBL:X62332; NID:g49906; PIDN:CAA44206.1; PID:g49907
A; Cross-references: EMBL:X62332; NID:g49906; PIDN:CAA44206.1; PID:g49907
A; Cross-references: EMBL:X62332; NID:g49906; PIDN:CAA44206.1; PID:g49907
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Best Local S
Matches 49
                                                                                  162 DGFQALQGIIHSIL------KKSCIE 181
                                                                                                                                                                                                                                                        109 DGELHEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPVN-----
                                                                                                                                                                                                                                                                                                                                               116 EVFSPPGSDRASFTKSLQGIRSFRRG--TFTDCALANMTQQIRQHVGKGVVNFAVVI--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                  49 TTLMKLTEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 NVYFVLDTSESVAMQSPTDSLLYHMQQFVPQFISQLQNEFYLDQVALSWRYGGLHFSDQV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DLYFILDKSGSV-----LHHWNE-IYYFVEQLAHKFISPQLRMSF----IVFSTRG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 11.2%;
Similarity 23.1%;
DSTEIDQDTINRIIKVMKHEAYGECYKVSCLE 263
                                                                                                                                                                     DGHVTGSPCGGIKMQABRAREEGIRLFALAPNRNLNEQGLRDIANSPHELYRNNYATMRP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LASKKDNEQHVFKVKD-MENLEDVFYQMIDES
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Pred. No. 0.48;
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: uniprot_sprot:*
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O9h6x2 homo sapien
O9c252 mus musculu
P58335 homo sapien
O6dfx2 mus musculu
O8bbq8 halocynthia
O9qye7 rattus norv
O8t6u5 mytilus edu
O8t5c3 mytilus edu
O8t5c3 mytilus gal
O04588 eimeria max
O60847 mus musculu
P11215 homo sapien
O8c6k9 mus musculu
P11394 gallus gall
O43981 eimeria ten
O9u8j9 neospora ca
O99715 homo sapien
P20702 homo sapien
P20702 homo sapien
P207035 mus musculu
O13349 homo sapien
O43853 homo sapien
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11.8	11.8	11.9 11.8	11.9	12.0	12.0	12.0	12.1	12.1	12.1	12.3	12.3
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Q9es77 mus musculu	Brue B	Q95li2 bos taurus Q91145 notophthalm				Q6dcq6 xenopus lae		Q21281 caenorhabdi	_	P34576 caenorhabdi	Q65zc2 caenorhabdi

ALIGNMENTS

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take N., Inagaki H., uchi S., Itoh T., Sh	Taliadani H., Macamade K., Kumiayar A., Taniyara S., Fukusumi I., Pujimori Y., Komiyama M., Tashiro H., Taniyami A., Fujiwara T., Ono T. Yamada K. Buiii V. Ozaki K. Hirao M. Ohmori V.	Goto Y., Shimizu F., Wakebe ., Takemoto M., Kawakami B., Takemoto M., Kawakami B.,	a H., Ichihara T., Shiohata N., San , Satoh N., Takami S., Terashima Y.	Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,	Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase TO.,	Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,	Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,	Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,	Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,	Yamamoto JI., Saito K., Kawai Y., Isono Y., Nakamura Y.,	Sekine M. Obavashi M. Nishi T. Shibabara T. Tanaka T. Ishii S.,	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamaton h Wayashi K Sato W Nacai K Kimura K Makita W	030.	SEQUENCE OF 184-564 FROM N.A. (ISOFORM 1), AND SEQUENCE FROM N.A. (ISOFORM 3).	[3]	"Identification of the certurar receptor for anthrax coxin.";	Bradley K.A., Mogridge J., Mourez M., Collier R.J., Young J.A.T.;	MEDLINE=21557240; PubMed=11700562; DOI=10.1038/n35101998;	[2] SEQUENCE FROM N.A. (ISOFORM 2), AND INTERACTION WITH ANTHRAX TOXIN.	Science 289:1197-1202(2000).	"Genes expressed in human tumor endothelium.";	, La	Traverso G., Romans K	MEDLINE=20407466; PubMed=10947988; DOI=10.1126/science.289.5482.1197;	A N WORE ED	±9606;	Eukaryota; metazoa; Chordata; Cranidta; vertebrata; Eutereostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Observation Control of the Control o	=ANTXR1; Synonyms=ATR, TEM8;	05-JUL-2004 (Rel. 44, Last annotation update)	2003	Q9H6X2; Q96P02; Q9NVP3; 28-FEB-2003 (Rel. 41, Created)	, p E	TLT 1

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REDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,
RX Altachell S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RX Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Lu X., Gibbs R.A.,
Raha S.S., Loquellano N.A., Peters G.J., Lu X., Gibbs R.A.,
Raha S.S., Loquellano N.A., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
VIllalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S.S., Loquellano J.W., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Raha S.S., Loquellano J.W., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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Raha S.S., Worley K.C., Hale S., Garcia B.M., Gay L.J., Hulyk S.W.,
Raha S.S., Loquellano J.W., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S.S., Loquellano J.W., Sodergren E.J., Lu X., Gibbs R.A.,
Raha S.S., Worley K.C., Hale S., Garcia B.M., Sanchez A.C., Grimwood J., Scheun J., Wersham R.,
Raha S.S., Worley K.W., Touchman J.W., Green B.D., Dickson M.C.,
Raha S.S., Worley K.W., Touchman J.W., Green B.D., D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
Hillman R. T., Green R.E., Brenner S.E.;
"An unappreciated role for RNA surveillance.";
Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
-I- FUNCTION: Cellular role is not yet known.
-I- SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis. Binding does not occur in the presence of calci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
MEDLINE=22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100;
Scobie H.M., Rainey G.J.A., Bradley K.A., Young J.A.T.;
"Human capillary morphogenesis protein 2 functions as an anthrax
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                         -!- TISSUE SPECIFICITY: Highly expressed in tumor endotheli-
but not in normal endothelial cells.
-!- DOMAIN: Binding to PA seems to be effected through the
-!- SIMILARITY: Belongs to the ATR family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete sequencing cDNAs.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event-Alternative splicing; Named isoforms=4; Comment=Experimental confirmation may be lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Natl. Acad.
                                                                                                                                                                                                                                                                                                                         IsoId=Q9H6X2-2; Sequence=VSP_000444, VSP_000445
                                                                                                                                                                                                                                                                                                                                                                                codon
                                                                                                                                                                                                                                                                                                                                                                                                      IBoId=Q9H6X2-1; Sequence=Displayed;
Note=May be produced at very low le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                IsoId=Q9H6X2-4;
                                                                                                                                                                                                                                                                       IsoId=Q9H6X2-3; Sequence=VSP_000446,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoforms;
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Oyama
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                                                                                                                                                                                                                                                                                                                                                                                mRNA,
                                                                                                                                                                                                                          Sequence=VSP_000448, VSP_000449;
                                                                                                                                                                                                                                                                                                                                                                              ed at very low levels due to a premature stop leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL NMD
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Pfam; PF000092; VWA; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
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EMBL; AF421380; AAL26496.1; --
EMBL; AK025429; BAB15128.1; AL
EMBL; AK001463; BAA91707.1; AL
EMBL; BC012074; AAH12074.1; --
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InterPro; IPR008399; Ant C.
InterPro; IPR002035; VWF A.
Pfam; PF05587; Anth Ig; 1.
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                                                   EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCI
                                                                                          IRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLPFYS
                                        EREANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSILKKSCI
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ilarity 100.0%;
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ALT_FRAME.
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Missing (In isoform 4
/FTId=VSP 000449.
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Pred. No. 9.2e-73;
); Mismatches 0;
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Missing (In isoform 2).
/FTId=VSP 000445.
NEKPFSVEDTYLLCPAPILKEVGMKAALQV -> SKSLQSP
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N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
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Extracellular (Potential).
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RESULT 2 ATR1_MOUSE ID ATR1_MOUSE

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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Vikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Vigi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Oi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikewa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hiraa A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
"Analysis of the mouse transcriptome based on functional annotation of
Tot Toth M., Shinade T., Ishi Y., Itoh M., Ragawa I.,
Analysis of the mouse transcriptome based on functional annotation of
                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Embryo; MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Anthrax toxin receptor 1 precursor (Tumor endothelial marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carson-Walter E.B., Watkins D.N., Nanda A., Kinzler K.W., St Croix B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Antxr1; Synonyme=Atr,
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Cellular role is not yet known. SUBUNIT: Binds to the protective antigen anthracis (By similarity).
                                                                                                                                                                                                                                                        SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                DOMAIN: Binding to PA seems (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         Note=No experimental confirmation
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                                                                                                                                                                                                                                                Belongs to the ATR fami
Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: Type I membrane protein
a license agreement (See http://www.isb-sib.ch/announce/
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Bell S.E., Mavila A., Salazar R., Bayless K.U., Ramayuru V., Maxwell S.A., Davis G.E.;

"Differential gene expression during capillary morphogenesis "Differential gene expression during capillary morphogenesis"
                                                                                                                                                                                                                                                                                                                   TATR2_HUMAN STANDARD;
P58335, Q86U11; Q8NB13; Q96NC7;
28-FBB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequ.
05-JUL-2004 (Rel. 44, Last anno
                                                                                                                                                                                                                                                                                              05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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DOMAIN
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                                                                                                                                                                                                          Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                         Name=ANTXR2; Synonyms=CMG2;
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Pfam, PF05586; Ant C; 1.
Pfam, PF00092; VWA; 1.
PROSITE; PS50234; VWFA; 1.
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InterPro; IPR008399; Ant C.
InterPro; IPR002035; VWF A.
Pfam; PF05587; Anth_Ig; 1.
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MGD; MGI:1916788; Antxr1.
                                                                                           MEDLINE=21539596; PubMed=11683410;
                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                       Mammalia; Eutheria;
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(Rel. 42, Last sequence update)
(Rel. 44, Last annotation updat
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                                                                                                                                                                                                                               (Human)
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N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
GRCINFTRVKNSQPAKYPLNNTYHDSSPPPAPIYTPPPPAP
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                                                                                                                                                                                       Catarrhini;
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6AC92049B4BB4F7C CRC64;
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekihe M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Yamamoto J.-I., Saito K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Yamamoto J.-I., Saito K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Pujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Moniyama H., Satoh N., Takama S., Terashima Y., Suzuki O.,
RA Matsugawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Pujimori Y., Kobatake N., Itakura S., Fukuzumi Y.,
RA Pujimori Y., Kobatake N., Itakura S., Fukuzumi Y.,
RA Rawabata A., Hikiji T., Kobatake N., Inagaki H., Itema Y., Okamoto S.,
RA Mizushima Sugano J., Satoh T., Shirai Y., Sasaki M.,
RA Mizushima S., Satoh T., Shirai Y., Nasaho Y., Nakagawa K.,
RA Mizushima S., Satoh T., Shirai Y., Masaho Y., Nakagawa K.,
RA Mizushima S., Satoh T., Shirai Y., Masuho Y., Yamashita R.,
RA Mizushima Sugano J., Satoh T., Shirai Y., Nakagawa K.,
RA Nakajasa T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
TCDMas. T., Satoh T., Shirai Y., Nakagawa K.,
RA Nakajasa T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
T., CDMas. T., Satoh T., Shirai Y., Nakagawa K.,
RA Nakagasa T., Satoh T., 
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J. Cell Sci. 114:2755-2773(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor.";
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Isoid=P58335-4; Sequence=VSP_008346;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed in colon, heart,
liver, peripheral blood leukocytes, placenta,
small intestine and spleen.
DOMAIN: Binding to PA seems to be effected thr
SIMILARITY: Belongs to the ATR family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Cellular role is not yet known.

SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis in a divalent cation-dependent manner, with the following preference: calcium > manganese > magnesium > zinc.

Seems to bind to collagen type IV and laminin.

SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).

Secreted (isoform 3). Isoform 1 is expressed at the cell surface while isoform 2 is predominantly expressed within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCE Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reticulum and not at the plasma membrane.
                                                                                                                                                                                                                                                                                                                                           Note=No
                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P58335-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P58335-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P58335-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                             Sequence=VSP_008344, VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence=VSP_008343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               splicing; Named isoforms=4;
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                                                                                                                                                                                                                                                                                                                                       confirmation available;
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olon, heart,
                                              through
                                                                                                                                                                                                                                                                                                                                                                                 008345
                                                                                                                               skeletal
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                                                  the VWA domain
                                                                                                                               muscle,
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EMBL; AY233452;

R EMBL; AK055636; BAB703.1,

R EMBL; AK051721; BAC03731.1;

Panew; HGNC:21732; ANTXR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
                                                                                         Q6DFX2;
25-OCT-2004
25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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CARBOHYD
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DOMAIN
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or send a
               Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                        Name=Antxr2;
                                                                           Anthrax toxin
                                                                                                                                                                     Q6DFX2
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InterPro; IPR002035; VWF_A.
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PF00092; VWA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                      SKGLEDLKRVSPVGETYIHEGLKLANEQI--QKAGGLKTSSIIIALTDGKLDGLVPSYAE
                                                                                                                                                                                                                                                              REANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSILKKSCIE
                                                                                                                                                                                                                                                                                                                                                             RQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSE
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489
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BAC03731.1; -.
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AAP04016.1;
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Chordata;
Rodentia;
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Last annotation updat
                                                                                                                                Created)
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Pred. No. 2.7e-38;
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TLDVSVSFNGGKSVISGSLIVTATECSNGIAAI
VTQAGVKWHDLTHCTFGLSGSGDPPTSAS (in
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Craniata; Ver
Sciurognathi;
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 Vertebrata; Euteleostomi;
chi; Muridae; Murinae; Mus
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A Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D.,
A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malak J.A., Gunaratne P.H.,
A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Pahey J., Helton E., Ketteman M., Madan A., Gobs R.A.,
Phale J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Philian M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Carlmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
A Jones S.J.
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR00839; Anth Ig.
InterPro; IPR008399; Ant C.
InterPro; IPR008399; Ant C.
InterPro; IPR008399; Ant C.
Pfam; PF05586; Anth Ig; I.
Pfam; PF05587; Anth Ig; I.
SMART; SM00327; VWA; I.
                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933430J11 product:hypothetical Proline-riched
Willebrand factor type A domain
                                                                                                                                                      Q8BVM2
Q8BVM2;
01-MAR-2003
01-MAR-2003
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"Generation and initial analysis of mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6;
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  mueculue
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                                                product:hypothetical Proline-rich region/von
lomain containing protein, full insert
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Pred. No. 4e-3
32; Mismatches
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  BMBL; AK077206; BAC36683.1; - Go; GO:0016021; C:integral to m GO; GO:0004872; F:receptor action interPro; IPR008400; Anth Ig. InterPro; IPR002035; VWF A. Pfam; PP05587; Anth Ig; I. Pfam; PF00092; VWA; I.
                                                                                                                                                                                                                                                                 STRAIN=C57BL/60, TISSUS=IEEELL,
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Fukuda S., Furuno M., Hanagqki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Kinczane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/63; TISSUE-Testis;

MEDLINB-20530913; PubMed=11076681; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
                        PRINTS; PRO0453; VWF.
SMART; SM00327; VWA;
                                                                                                                                                                                                                                                    Tomaru A., Toya T., Yasunishi A., Muramatsu M., Submitted (APR-2002) to the EMBL/GenBank/DDBJ d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
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[3]
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636;
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Mammalia; Eutheria; Rodentia;
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                                                VWFADOMAIN
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Carninci P.,

new

genes.";

IEA. IEA

databases.

Carninci P.,

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"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                      MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II Team;
                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cy full-length cDNA
303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                               DOI=10.1038/35055500;
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Best Local S
Matches 52
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Best Local
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                                                                                                                                      CHAIN
SEQUENCE
                                                                                                                                                                                                 SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                     Miyazawa S., Azumi K., Nonaka M.;
"Cloning and characterization of integrin alpha
solitary assidian, Halocynthia roretzi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Hemocyte;
MEDLINE=21103187; PubMed=11160215;
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SEQUENCE 64
                                                                                                                                                             SIGNAL
                                                                                                                                                                          PROSITE; PS50234; VWFA; 1. Cell adhesion; Integrin; S
                                                                                                                                                                                                                        PRINTS; PR01185; INTEGRINA. PRINTS; PR00453; VWFADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=HrITGA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Integrin alpha Hrl precursor.
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                                                                                                                                                                                                                                                                      InterPro; IPR000413; Integrin_alpha.
                                                                                                                                                                                                                                                                                       30; GO:0007229;
                                                                                                                                                                                                                                                                                              GO:0016021; C:integral to membrane, GO:0008305; C:integrin complex; IEA. GO:0005515; F:protein binding; IEA. GO:0007160; P:cell-matrix adhesion.
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                                      GFDLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQ
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1332
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641 AA; 7
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 24, Last annotation updat
                                                                                       Conservative
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                                                                                                                                                                Integrin;
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                                                                                            Score 146; Db 2,
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Pred. No. 9e-24;
                                                                                                                                     integrin alpha Hrl.
fW; 0D9108D2B05CFFAE CRC64;
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05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Integrin alpha-D precursor.
                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-!- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrin Lomains do not undergo protease cleavage.
-!- SIMILARITY: Belongs to the integrin alpha chain family.
-!- SIMILARITY: Contains 7 FG-GAP repeats.
  TRANSMEM
DOMAIN
                                                                                                                                                                                                                         EMBL;
                                                                                                           PRINTS; PR01185; INTEGRINA.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5.
SMART; SM00327; VWA; 1.
                                                                                                                                                            InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF A.
Pfam; PF01839; FGGAP; 3.
Pfam; PF00187; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                Repeat; Signal;
SIGNAL 1
                                                                        PROSITE; PS00242; INTEGRIN_ALPHA; PROSITE; PS50234; VWFA; 1.—Calcium; Cell adhesion; Glycoprote
                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallatin W.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley;
O'Brien M.M., VanderVi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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P11215; 1BHQ.
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Rodentia;
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to the EMBL/GenBank/DDBJ datab
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                                                                      Glycoprotein; Integrin; Magnesium; Receptor;
 Potential.
Cytoplasmic
                        Integrin alpha-D.
Extracellular (Potential)
                                                   Potential
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Sciurognathi;
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thi; Muridae; Murinae; Rat
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Matches 53
                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Proximal thread matrix protein 1 variant a.

Mytilus edulis (Blue mussel).
Eukaryota; Metazo; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.

NCBI TaxID-6550;
                                                                                                                                                                                                                                                                                                          Q8T6U5,
Q8T6U5,
01-JUN-2002
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MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903;

Sun C., Lucas J.M., Waite J.H.;

"Collagen-binding matrix proteins from elastomeric extrao byssal fibers";

Biomacromolecules 3:1240-1248(2002).

EMBL; AF414454; AAL83537.1; -.

GO; GO:0005198; F:structural molecule activity; IEA.
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GPFKR motif.

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01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2003 (TrEMBLrel. 24, Last annotation
Proximal thread matrix protein 1b.
Mytilus edulis (Blue mussel).
Bukaryota, Metazoa, Mollusca; Bivalvia; Pter
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22313036; PubMed=12425661; DOI=10.1021/bm0255903; Sun C., Lucas J.M., Waite J.H.; "Collagen-binding matrix proteins from elastomeric extrao byssal fibers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8T5C3
                                                                                                                                                                                                                                                                                                                                                                                                     Matrix protein. SEQUENCE 444
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0453; VWFADOMAIN
SMART; SM00327; VWA; 2.
PROSITE; PS50334; VWFA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomacromolecules 3:1240-1248(2002).
EMBL: AY053390; AAL17973.1; -.
GO; GO:0005198; F:structural molecul
InterPro; IPRO20035; VWF_A.
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                                                                                              DYSSKABIKGAID---KVTPSIIGQTAIGDGLENARLEV-FPNRNGGGREEVQKVVILLT
DGQNNGHKS---
                                    DGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPVNDGFQ
                                                                                                                                                                                                 DIAFVFDASSSINAMNPNNYGLMKDFMKDIVDRFNKTGPDGTQFAVVTFADRATKQFGLK 303
                                                                                                                                                                                                                                             DLYFILDKSGSV----LHHWNEIYYFVEQLAHKF--ISPQ-LRMSFIVFSTRGTTLMKLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIAFVFDASSSINANNPNNYGLMKDFMKDIVDRFNKTGPDGTQFAVVTFADRATKQFGLK 300
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PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-TTSSFN
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                                                                                                                                                                                                                                                                                               Score 139; DB 2;
Pred. No. 0.0012;
6; Mismatches 74;
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01-JUN-2002
01-JUN-2003
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 SEQUENCE FROM N.A. MEDLINE=93149203; Pul Pasamontes L.E., Hug
                                                                                                          Q04588 PRELIMINARY; PRT; 724 AA. Q04588; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Major antigen homologous sequence (emp100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00327; VWA; 2.
PROSITE; PS50234; VWFA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proximal thread matrix protein 1.
Mytilus galloprovincialis (Mediterranean mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005198; F:structural InterPro; IPR002035; VWF A. Pfam; PF00092; VWA; 2.
                                                    NCBI_TaxID=5804;
                                                                                  Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                 Eimeria maxima.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        3 DLYFILDKSGSV----LHHWNEIYYFVEQLAHKF--ISPQ-LRMSFIVFSTRGTTLMKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                           ALQGIIHSILKKSCI 180
                                                                                                                                                                                                                                                                                                       DGQNNGHKS----PEHESSLLRKEGVVIVAIGVGTGFLKSELINIASSEEYVF-TTSSFD
                                                                                                                                                                                                                                                                                                                                 DGEL--HEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIADSKDHVFPVNDGFQ 165
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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  PubMed=8426611; DOI=10.1016/0166-6851(93)90255-V;
Hug D., Huembelin M., Weber G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.48;
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Best Local S
Matches 53
  Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R.W., Olsen B.R., Nishimura I.;
"Structural variation of type XII collagen at its carboxyl-terminal NC1 domain generated by tissue-specific alternative splicing.";
J. Biol. Chem. 274:22053-22059(1999).
                                                                                                AND ALLE-2.
STRAIN-C578L/6J; TISSUE-Skin fibroblast;
MEDLINE-99348349; PubMed-10419532; DOI-10.1074/jbc.
Kania A.M.. Reichenberger E., Baur S.T., Karimbux k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q60847; P70322;
15-JUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation updat
Collagen alpha 1(XII) chain precursor.
                                                                                                                                                                                                                                                                                                                       MEDLINE=96170761; PubMed=8601036;
Boehme K., Li Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and short splice variants
collagen XII and their tissue-specific expression during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE CA1C_MOUSE
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SMART; SM00209; TSP1; 6.
SMART; SM00327; VWA; 1.
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HSSP; P07996; 1LSL.
GO; GO:0008083; F:gr
                                                                                                                                                                                                                                                                                                 development
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J, and Swiss Webster; TISSUE=Skin;
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Mammalia; Eutheria;
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Mus musculus (Mouse)
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InterPro; IPR000762; PTN MK.
InterPro; IPR000884; TSPI.
InterPro; IPR002035; VWF-A.
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                                                                                                                                                                                           AND XIIB-2
                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.4%; Score 136; DB 2
27.0%; Pred. No. 0.004;
tive 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Length 724;
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                                                                                                                                       .274.31.22053;
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                                                                                                           Taylor R.W.,
                                                                                                                                                                                                                                                                                                                       of mouse
embryonic
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INTERPRO; IPRO08160; Collagen.

INTERPRO; IPRO0896; ConA like lec_gl.

DR InterPro; IPRO0896; FN III.

DR InterPro; IPR003957; FN III.-like.

DR InterPro; IPR003129; TSP_N.

DR InterPro; IPR003129; TSP_N.

Pfam; PF00139; Collagen; 5.

R Pfam; PF000041; fn3; 18.

R Pfam; PF00210; TSP N. **

PFam; PF00210; TSP N. **
PRINTS; PRO0453; VWFADOMAIN.

SMART; SM00060; FN3; 18.

SMART; SM002210; TSPN; 1.

SMART; SM00327; VWA; 4.

PROSITE; PS50853; FN3; 18.

PROSITE; PS50234; VWA; 4.

Alternative splicing; Cell adhesion; Collagen; Extracellular matrix; Glycoprotein; Hydroxylation; Repeat; Signal; Structural protein.

SIGNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U25652; AAA99719.1;
EMBL; U57095; AAB07047.1;
HSSP; P18614; 1MHP.
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SIMILARITY: Belongs to the fibril-associated collagens with interrupted helices (FACIT) family.

SIMILARITY: Contains 18 fibronectin type III domains.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId Q60847-4; Sequence VSP 001150, TISSUE SPECIFICITY: Highest expression Skin, cornes, sclers, blood vessels, ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrillar matrix (By similarity). SUBUNIT: Trimer of identical chains each containing 190 kDa of nontriple-helical sequences (By similarity). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
PTM: O-glyco
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Name=XIIA-2; Synonyms=ER#K;
IsoId=Q60847-2; Sequence=VSP_001151,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=4; Comment=The final tissue form of collagen XII homotrimers or any combination of the various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q60847-3; Sequence=VSP_001150;
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                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-88857215; PubMed=2454931; DOI=10.1083/jcb.106.6.2153;
Arnaout M.A., Gupta S.K., Pierce M.W., Tenen D.G.;

"Amino acid sequence of the alpha subunit of human leukocyte receptor Mol (complement receptor type 3).";

J. Cell Biol. 106:2153-2158(1988).
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Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha
subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor Neutrophil adherence receptor).
Name=ITGAM; Synonyms=CD11B, CR3A;
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Mammalia; Eutheria;
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subunits and a calcium binding site on its lower surface.",
Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875 (1998).
-I- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
adhesive interactions of monocytes, macrophages and granulocytes
as well as in mediating the uptake of complement-coated particles.
It is identical with CR-J, the receptor for the iC3b fragment of
the third complement component. It probably recognizes the R-G-D
peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
fibringen, factor X and ICAM1. It recognizes Pl and P2 peptides
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MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8;
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MEDLINE=9363671; PubMed=8747460; DOI=10.1016/S0969-2126(01)00271-4;
Lee J.O., Banketon L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway fo
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MEDLINE=95171458; PubMed=7867070; DOI=10.1016/0092-8674(95)90517-0;
Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
"Crystal structure of the A domain from the alpha subunit of integr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87076671; PubMed=3539202; DOI=10.1016/0167-48 Pierce M.W., Remold-0'Donnell E., Todd R.F. III, Arna "N-terminal sequence of human leukocyte glycoprotein across species and homology to platelet IIb/IIIa."; Biochim. Biophys. Acta 874:368-371(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pahl H.L., Rosmarin A.G., Tenen D.G.; "Characterization of the myeloid-specific Blood 79:865-870(1992).
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"Experimental support fo
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                                with I-domains do not undergo prote SIMILARITY: Belongs to the integrin SIMILARITY: Contains 7 FG-GAP repea SIMILARITY: Contains 1 VWFA domain.
                                                                                                  associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane prote:
TISSUE SPECIFICITY: Predominantly expressed
granulocytes.
DOMAIN: The integrin I-domain (insert) is a
                                                                                                                                                                                         of fibrinogen gamma chain.
SUBUNIT: Heterodimer of an alpha
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NOTE=CD guide
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                                                                                                                                                                                                                                                                                                                                                                                                                       DOI=10.1073/pnas.95.9.4870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOI=10.1016/0167-4838(86)90037-3;
Todd R.F. III, Arnaout M.A.;
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SMART; SM0034; vna, ...
PROSITE; PS00242; INTEGRIN ALPHA; 1.
PROSITE; PS50234; VWFA; 1.
3D-structure; Calcium; Cell adhesion; Direct
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                                                                      SMART; SM00191; Int_alpha; 5.
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PRINTS; PRO0453; VWFADOMAIN.
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CHAIN
                                          SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUB=Ovary;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN fullength enriched library, clone:E330019B14 product:hypothetical willebrand factor type A domain containing protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meth.
                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Ovary;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Ovary;
MEDLINE=99279253; PubMed=10349836; DOI=10.1016/S0076-6879(99)03004-9;
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Eukaryota, Metazoa,
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  SEQUENCE FROM
                                                                                                                                                                                                                                                               Nature
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSI The FANTOM Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=E330026B02Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lonal annotation of a full-length mouse cDNA collection.";
409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNN-FEALKTIQNQLREK 331
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     N.A.
                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
1152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Integrin alpha-M
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                                                                                                                                                                                                                                                                                                                                             Group
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on functional
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                                                                                                                                                                                                                                                                                                                                             Team;
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                                                                      genes.";
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RESULT 15
CAIC CHICK STANDARD;
ID CAIC CHICK STANDARD;
AC P1394; Q04509;
AC P13941; Q04509;
AC P1397 (Rel. 35, La
DT 01-NOV-1997 (Rel. 45, La
DT 25-OCT-2004 (Rel. 45, La
DE Collagen alpha 1(XII) ch
GN Name=COL12A1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Choi
OC Archosauria; Aves; Neogr
OC Gallus.
OX NCBI_TaxID=9031;
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A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohasto N., Okazaki Y.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohasto N., Sazaki Y.,

A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AKO54356; BAC35749.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ...USITE; PS50234; VWFA; 6.
Hypothetical protein.
SEQUENCE 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wattahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Vanaka Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
                                                            Gallus gallus (Chicken)
Eukaryota; Metazoa; Cho
                                          Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002035; VWF_A. Pfam; PF00092; VWA; 6.
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STRAIN=C57BL/6J; T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REQIROGLEELOKVLPGGDT----YMHEGFERASEQIYYENRQGYRTASVIIALTDG
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                                                                                                                                                                                                                                                                                                                                                                                 MSRDSVL----GPAHKLREENIRVHAIGVKEANQTQLREIAGEEKRVYYVHE-FDALRNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPDLGKAIENIRQM--GGNTNTGAALNFTLKLLQRAKKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIYLLIDGSGSTQPTDFHEMKTFLSEVVGMFNIAPHKVRVGAVQYADTWDLEFEISKYSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Ovary;
a K., Akimura T., Arakawa T.,
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                                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                              , Last sequence upo
, Last annotation u
) chain precursor
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Pred. No. 0.026;
9; Mismatches
                                            Craniata; Vertebrata; ; Galliformes; Phasian:
                                                                                                                                                                                                               PRT;
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                                                                                                                                                         update
                                                                                                                    update)
(Fibrochimerin)
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                                          Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            - RGSKVPCHLVVLTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci P.,
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MEDLINE-9370352; PubMed=7642694; DOI=10.1083/jcb.130.4.1005;
MEDLINE-9370352; PubMed=7642694; DOI=10.1083/jcb.130.4.1005;
MCOCH M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet
"Large and small splice variants of collagen XII: differential
expression and ligand binding.";
J. Cell Biol. 130:1005-1014(1995).
-!- FUNCTION: Type XII collagen interacts with type I collagen-
containing fibrils, the COLl domain could be associated with
surface of the fibrils, and the COL2 and NC3 domains may be
localized in the perifibrillar matrix.
-!- SUBUNIT: Trimer of identical chains each containing 190 kDa o
nontriple-helical sequences.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=White leghorn;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gordon M.K.,
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                            - PTM: The triple-helica
each end.
- PTM: Prollines at the t
unit (G-X-Y) are hydro
- PTM: O-glycosylated; g
(By similarity)
- SIMILARITY: Belongs to
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                                                                                                                                                                                                                                ligaments, perichondrium, and periosteum, al tissues containing type I collagen.

DOMAIN: This sequence defines five distinct helical domains (COL1 and COL2) and three no domains (NC1, NC2, and NC3).

PTM: The triple-helical tail is stabilized between the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of the triple of triple of the triple of the triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple of triple o
                                                                                                                                                                                                                                                                                                                                                                                                Name=Short;
IsoId=Pl3944-2; Sequence=VSP 001148;
TISSUB SPECIFICITY: Type XII collagen is present in tendons,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2; Comment=The final tissue form of collagen XII may contain homotrimers of either isoform Long or isoform Short or any combination of isoform Long and isoform Short. Only isoform is a proteoglycan. Isoform Long has more restricted expressin embryonic tissue than isoform Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P13944-1; Sequence=Displayed;
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                                                                                                                                Prolines at the third position of the (G-X-Y) are hydroxylated in some or al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ဝ္
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to the fibril-associated (FACIT) family.
                                                                                                glycosaminoglycan
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molecule with partial homology
                                                                                                       of chondroitin-sulfate
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nontriple-helical
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InterPro; IPR008160; Collagen.

R InterPro; IPR008985; ConA like_lec_gl.

R InterPro; IPR003961; FN III-like.

R InterPro; IPR003957; FN III-like.

R InterPro; IPR003129; TSP N.

R InterPro; IPR003129; TSP N.

R InterPro; IPR003129; TSP N.

R Pfam; PP01391; Collagen; 4.

R Pfam; PP02210; TSP N; 1.

R Pfam; PP02210; TSP N; 1.

R Pfam; PP00032; VWA; 4.

R PRNSITS; PM00327; VWA; 4.

R PROSITE; PS50833; VWPA; 4.

R PROSITE; PS50834; VWPA; 4.

Alternative splicing; Cell adhesion; Collagen;

Hydroxylation; Repeat; Signal; Extracellular matrix; Glycoprotein;

Hydroxylation; Repeat; Signal; Extracellular matrix; Glycoprotein;

Hydroxylation; Repeat; Signal; Extracellular matrix; Glycoprotein;

Hydroxylation; Repeat; Signal; Extracellular matrix; Glycoprotein;

Hydroxylation; Repeat; Signal; Extracellular matrix; Glycoprotein;
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EMBL; X61024; CAA43358.1; -.
EMBL; M17375; AAA48718.1; -.
EMBL; J05137; AAA48635.1; -.
EMBL; X67327; CAA47744.1; -.
PIR; A40020; A40020.
HSSP; P56199; 1QC5.
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                                                                                                                                         Contains 18 fibronectin type III domains. Contains 1 TSP N-terminal (TSPN) domain. Contains 4 VWFA domains.
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Collagen alpha 1(XII) chain.
Fibronectin type-III 1.
                                                                               imperfection.
Nonhelical region (NC2).
Triple-helical region (C
                                                                                                                                  VWFA 4.
TSP N-terminal.
Nonhelical region (NC3)
Triple-helical region (
Nonhelical region (NC1).
Asp/Glu-rich (acidic).
Arg/Lys-rich (basic).
Cell attachment site (Potential).
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Fibronectin
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                                               LFFYSERBANRSRDLGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGIIHS
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                                                               DKAQALGALQNVQ--YRGGNTRTGKALTFIKEKVLTWESGMRRGVPKVLVVVTDGRSQDE
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Search completed: June 13, 2005, 20:03:17 Job time : 61.7608 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Regult No.	Score	Query Match	Length	BQ	ID	Description
1	668	100.0	297	. ۔	AAM38976	Aam38976 Human pol
N	899	8	328	7	0	8 Human
ω	899	100.0	328	7	ADM64584	Human
4.	899	100.0	333	w	AAB01422	Human
(J)	899	8	333	S	ABP54905	
o	899	100.0	333	7	ADI00534	
7	668	100.0	333	7	ADM64568	Human
8	668	•	342	7	ADI00554	Human
9	668	00.	342	7	ADM64580	Adm64580 Human TAN
10	668	100.0	345	7	ADI00556	
11	899	100.0	345	7	ADM64582	Adm64582 Human TAN
12	668		368	υ	ABP54903	
13	899	100.0	384	7	ADM64586	Adm64586 TANGO197
14	899	•	403	4.	AAE01439	Human
15	899	•	403	σ	ABG63874	
16	899	100.0	403	8	ADL77139	Adl77139 Albumin f
17	899	100.0	460	7	ADI00562	Adi00562 Human TAN
18	899	100.0	460	7	ADI00560	Human
19	668	100.0	479	7	ADI00564	
20	668	100.0	504	7	ADI00566	Adi00566 Human TAN
21	899	100.0	529	7	ADI00568	Human
22	899	100.0	538	7	ADE97421	Ade97421 Human chi
23	899	100.0	540	7	ADI00544	Human
24	899	100.0	540	7	ADM64588	-
25	899	100.0	549	7	ADI00546	Adi00546 Human TAN

WPI; 2001-442253/47. N-PSDB; AAI58132.

Example 4; SEQ ID NO 2121; 10078pp; English.

Novel nucleic acids and polypeptides, useful for treating disorders as central nervous system injuries.

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Abb90785	Abb90731	Ad177138	Abg63873	Aae01469	Adr48216	Adm64578	Adj70017	Adi00552	Abu54431	Abu54457	Abp54904	Abb90724	Abb90750	Adm64576	Adi00550	Adm64592	Adm64590	Adi00548	Adi00542
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20-JUN-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's, Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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; 2000US-00488725;
; 2000US-00552317;
; 2000US-00598042;
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New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing cameliorating symptoms of anthrax comprises a von Willebrand factor
                                                                                                        WPI; 2003-720708/68
N-PSDB; ADI00557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion; von Willebrand factor A-like domain; vWF; antibacterial; cutaneous; inhalation anthrax; human; TANGO 197 HisTag fusion; mutant;
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                                                                                                                                                                                                            Rottman JB,
                                                                                                                                                                                                                                                                                                                    (OKEE/)
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                                                                                                                                                                                                                                                                         ROTTMAN J B.
O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
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                                                                                                                                                                                                                                                                                         (ROTT/) ROTTMAN J B.
(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 HiaTag fusion protein of the invention.
                           New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing camelicating symptoms of anthrax comprises a von Willebrand factor domain (vWF) amino acid sequence and an amino acid sequence heterol to the vWF.
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von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; human; TANGO197; his tag; fusion protein.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                    TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; Crohn's disease; chronic myelogenous leukemia; cancer; liver disease; Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia; autoimmune disease; myasthemia gravis; autoimmune disease; myasthemia gravis; autoimmune disease; prognosis; systemic lupus erythematosus; transgenic animal; diagnosis; prognosis; prophylatic; therapeutic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF. Also described as method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a fusion protein comprising mature human TANGO197, thrombin cleavage site and his tag that can be used to treat exposure to or
               Novel nucleic acid sequences encoding TANGO-128, 140, 19 and 239 polypeptides useful for the treatment of asthma, arthritis, psoriasis and autoimmune diseases.
                                                                                   WPI; 2000-465743/40.
N-PSDB; AAA47455.
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Pred. No. 2.7e-92;
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                                                            WPI; 2002-713235/77.
N-PSDB; ABV73883.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JAN-2003
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                                                                                                                                                                                                                                                                                05-DEC-2000; 2000US-0251481P
                                                                                                                                                                                                                                                                                                                                          03-OCT-2001; 2001WO-US030941
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leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis,
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/label= Mature_protein
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Novel isolated polypeptide useful for identifying agent that prevents or

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  WPI; 2003-720708/68
                                                      Rottman
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nimal suffering
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibacterial; gene therapy;
von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWP. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous to the vWF.
New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing ameliorating symptoms of anthrax comprises a von Willebrand factor
                                                                               N-PSDB; ADM64567.
                                                                                                                                                                                                                                        (ROTT/)
(OKEE/)
(OZKA/)
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TANGO 197 protein of the invention.
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                                                                                                                                                            O'keefe
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                                                                                                                                                      Ozkaynak
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Pred. No. 2.8e-92;
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Best Local &
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                                                                                                                                                                                                                                                            (ROTT/)
(OKEE/)
(OZKA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain
to the
New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing ameliorating symptoms of anthrax comprises a von Willebrand factor domain (vWF) amino acid sequence and an amino acid sequence hetero
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human TANGO 197 FLAG fusion protein - plasmid po613.
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DB; ADI00553.
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                                                                                                                                                                                                                              ) ROTTMAN J B.
) O'KEEFE T L.
) OZKAYNAK E.
) HEALEY J J.
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                                                                                                                                                                                 O'keefe
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Pred. No. 2.8e-92;
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                                                                                                                                                                                 Healey
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                                                                                                                                                                                                                                                                                                                      antibacterial; gene therapy;
von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
vWF amino archax; human; TANGO197; FLAG; fusion protein; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWP. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or ameliorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 FLAG fusion protein of the invention.
                                              New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                  N-PSDB; ADM64579.
                                                                                               WPI; 2003-829643/77
                                                                                                                                                                    (ROTT/)
                                                                                                                                                                                                                                                                              US2003134786-A1
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                   Human TANGO197-FLAG epitope
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                                                                                                                     Rottman JB,
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                                                                                                                                                          (OZKA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113
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                                                                                                                                           ROTTMAN J B.
O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein; 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGLEBLQKVLPGGDTYMHBGFBRASBQTYYBNRQGYRTASVIIALTDGBLHBDLFFYSBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLYFILDKSGSVLHHWNBIYYFVBQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 AA;
                                                                                                                     O' keefe
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                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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                                                                                                                     Ozkaynak E,
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Pred. No. 2.9e-92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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XX fusio
XX Cutan
XX Flomo
OS Synth
XX Plasm
OS Synth
XX Homo
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XX Homo
OS Synth
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New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing cameliorating symptoms of anthrax comprises a von Willebrand factor
                                                                                        WPI; 2003-720708/68.
N-PSDB; ADI00555.
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Synthetic.
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plasmid pO
                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-2002; 2002US-00201292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion; von Willebrand factor A-like
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                                                                                                                                                                                     Rottman
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                                                                                                                                                                                                                                       ROTTMAN J B.
O'KEEFE T L.
OZKAYNAK E.
HEALEY J J.
                                                                                                                                                                                 JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      us; inhalation anthrax; pO614; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
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                                                                                                                                                                                 O'keefe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild-type Cys replaced by Ser followed
thrombin cleavage site and His tag"
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                                                                                                                                                                                 Ozkaynak E,
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Pred. No. 2.9e-92;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain; vWF; antibacterial;
; TANGO 197 HisTag fusion; m
                                                                                                                                                                                 Healey
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RESULT 11
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(OKEE/) O'KEEFE T L.
(OZKA/) OZKAYNAK E.
(HEAL/) HEALEY J J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel fusion polypeptide comprising a von Willebrand factor A-like domain (vWP) amino acid sequence and an amino acid sequence heterologous to the vWP. The polypeptide of the invention demonstrates antibacterial activities whilst the composition and method may be useful in preventing or amellorating the symptoms of cutaneous and/or inhalation anthrax. The current sequence is that of the human TANGO 197 HiaTag fusion protein of the invention.
                       New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing amellorating symptoms of anthrax comprises a von Willebrand factor domain (WF) amino acid sequence and an amino acid sequence hetero to the vWF.
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N-PSDB; ADM64581.
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von Willebrand factor A-like domain amino acid sequence;
vWF amino acid sequence; anthrax; Bacillus anthracis; cutaneous anthrax;
inhalation anthrax; human; TANGO197; his tag; fusion protein; gene.
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                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human anthrax toxin receptor
Region
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                                                                                                                                                                                                                       Domain
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 motif with amino
                                                              motif with
                                                                                                            motif with
                                                                                                                                                     /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 52, 54, 118 and 150"
                /note= "forms metal ion-dependent adhesion site (MIDAS) motif with amino acid residues 50, 52, 54 and 150"
                                                            /note= "forms metal ion-dependent
motif with amino acid residues 50,
                                                                                                                           /note=
                                                                                                                                                                                                                                                                                             /note= "PA-binding fragment, begins at any amino acid in the range 27-43 and ends at any amino acid in the range 221-321, region specifically described in Claim 3"
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                       notes
                                                                                                                                                                                                                                                                 label Mature_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the protein sequence of a human surface-bound anthrax toxin receptor (ATR), as predicted from an isolated CDNA clone. Anthrax toxin protective antigen (PA) binds to the ATR at a von willebrand factor A domain located in the extracellular domain of ATR. The invention provides ATR polypeptides and polynucleotides, vectors, host cells, and transgenic and knock-out animals. It also provides methods for identifying molecules that bind the ATR and which reduce the coxicity of anthrax toxin. A claimed method for treating anthrax in a human or animal involves administering an agent that inhibits binding between PA and ATR at a level effective to reduce the severity of anthrax. Suitable agents include ATR or a PA-binding fragment of ATR, a PA-binding polypeptide at least 80% identical to these, a fusion protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a monoclonal or
nucleic acid
antibacterial; gene therapy;
                                                          TANGO197 extracellular domain-mutant
                                                                                                                     03-JUN-2004
                                                                                                                                                                                                                                       ADM64586 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human animal suffering from anthrax.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABV73881.
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                                                                                                                                                                                                                                                                                                                                                                                     EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
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                                                                                                                  (first entry)
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Pred. No. 3.2e-92;
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                                                       fusion protein
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RESULT 14
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Best Local S
Matches 173
                               17-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a fusion polypeptide comprising a von Willebrand factor A-like domain (wwF) amino acid sequence and an amino acid sequence heterologous to the wWF. Also described are: a method of preventing or ameliorating a symptom of anthrax in a subject thought to be at risk for exposure to or suspected of having been exposed to Bacillus anthracis; and a pharmaceutical composition comprising the novel fusion polypeptide. The composition and method are useful in preventing or ameliorating symptoms of cutaneous and/or inhalation anthrax. This is the amino acid sequence of a fusion protein comprising human TANGO197 extracellular region, minus the DG residues closest to the transmembrane region, and immunoglobulin G (IGG) fragment of crystallisation (FC) with mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New TANGO 197 and/or TANGO 216 fusion polypeptides for preventing or ameliorating symptoms of anthrax comprises a von Willebrand factor A-like domain (vWF) amino acid sequence and an amino acid sequence heterologous
                                                                                           AAE01439;
                                                                                                                                             AAE01439 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 44; SEQ ID NO 10; 64pp; English
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DB; ADM64585.
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OZKAYNAK E.
HEALEY J J.
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immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; cell culture; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemocraxis; food additive; gene therapy; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secreted protein; proliferative disorder; cancer; tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental abnormality;
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Protein
                                  Peptide
            /label= Signal_peptide
                                   Location/Qualifiers
/note= "Mature human secreted protein"
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WO200134626-A1.

17-MAY-2001.

05-NOV-1999; 99US-0163581P. 30-JUN-2000; 2000US-0215133P. 01-NOV-2000; 2000WO-US030045

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Komatsoulis GA, Moore PA, Birse É Z.

2001-308778/32.

New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives. and

Claim 11; Page 485-486; 562pp; English.

CC AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted CC protein genes, and AAE0146-AAE01513 represent the proteins they encode. CC AAE01514-AAE01544 represent human secreted protein fragments or variants. CC The genes and their secreted proteins are useful for preventing, treating cor ameliorating medical conditions, e.g., by protein or gene therapy. CC Pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the 28 genes, the new genes. Specific uses are described for each of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, cc cognitive disorders, schizophrenia, asthma, skin disorders (e.g., cognitive disorders, schizophrenia, asthma, skin disorders, cardiovascular disorders, cognitive disorders, endocrine disorders, gastrointestinal disorders, cognificated disorders, endocrine disorders, and include cognistic transplantation, for supporting cell culture of primary tissues, cordiopance tissues, to identify their cognate ligands or binding parterion of the invention can be used to all wound healing and epithelial cell correction of the invention can be used in allevateing symptoms associated correction of the invention a human secreted protein of the invention can be used in macrote to filmunoassays e.g., cardioimmunoassays or enzyme linked immunoasorbent assay (ELISA). The invention can be used in allevatein of the invention represents a human secreted protein of invention

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Sequence

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Query Match

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AC ABGG3
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The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HAA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitie), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrined so (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, haematopoietic disorders, neural disorders (e.g. Alzheimer's, meningitis, parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                       New fusion protein for treating disease e.g. diabetes comprises albumin fused to a therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-APR-2000; 2000US-0229358P
25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
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                                                                                                                                                                                                                                                                                                                                                                                      Claim
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Patent No. 5470953
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5470953el Human
NUMBER OF SEQUENCES: 51
                                                           Query Match 15.4%;
Best Local Similarity 28.3%;
Matches 52; Conservative 30
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/173,497
PILLING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: P38,659
REFERENCE/DOCKET NUMBER: 27866/32168
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall,
                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
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TELEX: 25-3856
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E: Marshall, O'Toole, Gerstein, Murray & Borun 233 South Wacker Drive, 6300 Sear Tower
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                                                               36; Mismatches
                                                             Score 138.5; DB 1;
Pred. No. 6.6e-07;
6; Mismatches 71;
                                                                                                      Length 1151;
                                                               Indels 25;
                                                                  Gaps
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                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-618-37
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US-08-485-618-37
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                                                                           Query Match 15.4%; Score 138.5; DB 1; Best Local Similarity 28.3%; Pred. No. 6.6e-07; Matches 52; Conservative 36; Mismatches 71;
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                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr. Joseph A.
REGISTRATION NUMBER: 27866/3279:
REFERENCE/DOCKET NUMBER: 27866/3279:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                            TELEPHONE: 312-474-0448
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CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United
ZIP: 60606-6402
                                                                                                                                                                                                                                   LENGTH:
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142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
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233 South Wacker Drive, 6300 Sear Tower
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Best Local Similarity
Matches 52; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/3239:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS LENGTH: 1151 amino ac:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-DEC-1993 PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 08/173,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
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STATE: Illino
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TELEFAX: 312-474-0448
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                                                                                                                                142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
114 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI----ADSKDHVFPVNDGFQA 164
                                             202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
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                                                                                                                                                                                                                 15.4%; Score 138.5; DB 1 ilarity 28.3%; Pred. No. 6.6e-07; Conservative 36; Mismatches 71
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US-08-605-672-37
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Matches
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PILING DATE: 21-DEC-122.

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/

TELECOMMUNICATION INFORMATION:

"ET.RPHONE: 312-474-6300
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Best Local &
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 amino acids
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

APPLICATION DATE: 21-DEC-1994

21-DEC-1994
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APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312-474-0448
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TELEX: 25-3856
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STREET: 233 South Wacker Drive, 6300 Sear Tower
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                                     114 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFFVNDGFQA 164
                                                                           202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSÄKKILLVITDGQKYRD 256
                                                                                                                                                     142 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 201
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52; Conserv
                                                                                                                                                                                        1 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
 PLEYSDVI PAADKA---GIIRYAI GVGDAFQEPTALKELNTI GSAPPQDHVFKVGN-FAA
                                                                                                               DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED
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                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                            15.4%; Score 138.5; DB 2; Length 1151; 28.3%; Pred. No. 6.6e-07; tive 36; Mismatches 71; Indels 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Williams Jr., JOSEDH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 23-DEC-
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
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                                                                                                                                                                                                                                                                                                                                                                                 TYPE: ami
                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 312-474-0448
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GY: linear
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 LQGI 168
                                       PLBYSDVI PAADKA---
                                                                                                               DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
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                                         -GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA 312
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PPLICATION NUMBER: US/08/943 767
PILING DATE:
CLASSTEE.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY,AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
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SEQUENCE CHARACTERISTICS
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
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313
                                     165 LQGI 168
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GY: linear
LRSI 316
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28.3%; Pred. No. 6.6e-07;
tive 36; Mismatches 71; Indels 25;
                                                                                                                                                         GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
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APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 6432404el Human Beta-2
FILE REFERENCE: 27866/36646
CURRENT APPLICATION NUMBER: US/09/688,307A
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 09/199,043
PRIOR FILING DATE: 1998-11-16
PRIOR PPLICATION NUMBER: 08/65,672
PRIOR FILING DATE: 1996-02-22
PRIOR FILING DATE: 1996-02-25
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR APPLICATION NUMBER: 08/286,889
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
PRIOR FILING DATE: 1994-08-05
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; Sequence 37, Application US/09688307A
; Patent No. 6432404
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SOFTWARE: PatentIn Ver.
SEQ ID NO 37
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EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER FILING DATE: 1997-10-03
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EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-08-05
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APPLICANT: Van der Vieren,
TITLE OF INVENTION: No. 62
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CURRENT APPLICATION NUMBER: US/09/193,043
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FILING DATE: 1994-12-21
APPLICATION NUMBER: 08/943,363
FILING DATE: 1997-10-03
                                                                APPLICATION NUMBER: 08/362,652
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; Pred. No. 6.6e-07
36; Mismatches 7:
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Gaps

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GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: Gallatin, Michael W.
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 662091561 Human 2
FILE REFERENCE: 27866/35004
CURRENT APPLICATION UNMBER: US/09/350,259
CURRENT FILING DATE: 1999-07-08
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER APPLICATION NUMBER: 09/193,043
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER PILING DATE: 1994-08-05
EARLIER FILING DATE: 1994-08-05
EARLIER PILING DATE: 1994-12-21
EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 37
LENGTH: 1151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.4%; Score 138.5; DB 4; Best Local Similarity 28.3%; Pred. No. 6.6e-07; Matches 52; Conservative 36; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/09350259 Patent No. 6620915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 361
COTHER INFORMATION: Xaa =
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1118
OTHER INFORMATION: Xaa = any or unknown amino acid
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LOCATION: 1117
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LOCATION: 506
OTHER INFORMATION: Xaa =
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LOCATION: 486
OTHER INFORMATION: Xaa =
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ORGANISM: Rattue rattue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 464
OTHER INFORMATION: Xaa =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 LRSI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 LQGI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 PLEYSDVIPAADKA---GIIRYAIGVGDAFQEPTALKELNTIGSAPPQDHVFKVGN-FAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
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; TYPE: PRT; ORGANISM: Rattus rattus US-09-350-259-37
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US-08-485-618-55
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GENERAL INFORMATION:
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Best Local Similarity 28.3%; Pred. No. 6.6e-07;
Matches 52; Conservative 36; Mismatches 71
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                SEQUENCE CHARACTERISTICS
LENGTH: 1161 amino aci
                                                                                                                                                                                 REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/32797
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                    FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
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CORRESPONDENCE ADDRESS:
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 233 Sout
CITY: Chicago
STATE: Illinois
                       TYPE: amino acid
TOPOLOGY: linear
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CLASSIFICATION:
                                                                                                                                                         TELEFAX:
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                                                                   1161 amino acids
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                                                                                                                                                           312-474-0448
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RESULT 11
US-08-362-652-55
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                                                                                                                                         TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENCTH: 1161 ami-
    Matches
                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 55, Application US/08362652 Patent No. 5766850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

ATTORNEY/ACENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REGISTRATION NUMBER: 38,659
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APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sear Tower
                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                     TELEPHONE: 312-474-63
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States ZIP: 60606-6402
                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 LQGI 168
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    Similarity 28.3
52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                                                                                                                           1161 amino acids
                                                                                                                        linear
                                                                                                                                                                                                                                                          312-474-6300
                                                                                              protein
15.4%; Score 138.5; DB 1; 28.3%; Pred. No. 6.7e-07; tive 36; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.4%; Score 138.5; DB 1; Length 1161; 28.3%; Pred. No. 6.7e-07;
                                                                                                                                                                                                                                                                                                             38,659
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Gaps
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                                 Query Match
Best Local S
Matches 52
                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 ami-
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APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5817515el Human
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
US 08/173,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,672
                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                      NAME: Williams Jr., Joseph A. REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 233 Sc
CITY: Chicago
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                                 52;
1 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                      Similarity
                                                                                                                                                   amino acid
GY: linear
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233 South Wacker Drive, 6300 Sear Tower
                                     Conservative
                                                                                                                               protein
                                                     28.3%;
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                                     36;
                                 Score 138.5; DB 2
Pred. No. 6.7e-07;
6; Mismatches 71
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                                                                      DB 2;
                                   Indels
                                                                    Length 1161;
                                 25;
                                 Gape
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US-08-482-293A-55
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GENERAL INFORMATION:
                                                                           Matches
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                 TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
PILING DATE: 21-DEC-1994
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1161 amino acids
                                                                                                                                                                                                                                                                                                                                                                 PILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
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APPLICANT: Van der Vieren, Monica
TTTLR OP INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/173,497
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                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
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CLASSIFICATION: 530
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STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                         TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                           52;
                                   1 plyfildksgsv-lhhwneiyyfveqlahkfispqlrmsfivfstrgttlmklte----
DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 211
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                                                                           Conservative
                                                                                                                                                                     protein
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                                                                     15.4%; Score 138.5; DB 2;
28.3%; Pred. No. 6.7e-07;
28.3%; Mismatches 71;
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                                                                           Indels
                                                                                                             Length 1161;
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Patent No. 5837478
                                                                                                               Matches
                                                                                                                                 Best Local Similarity
                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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CITY: Chicago
CITY: Illinois
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TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
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                                   152 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL 211
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55 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 113
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                                                                       DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTE----
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                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marshall, O'Toole, Gerstein, Murray & Borun
3 South Wacker Drive, 6300 Sear Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US 08/362,652
21-DEC-1994
                                                                                                         15.4%; Score 138.5; DB: 28.3%; Pred. No. 6.7e-07 tive 36; Mismatches 7.
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                                                                                                                                                   DB 2;
                                                                                                                                                   Length 1161;
                                                                                                               Indels
                                                                                                             25;
                                                                                                             Gaps
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Sequence 55, Application US/09193043
Patent No. 6251395
GENERAL INFORMATION:
APPLICANT: Gallatin, Michael W.
APPLICANT: WIN MICHAEL W.
TITLE OF INVENTION: No. 6251395el Human 2
FILE REFERENCE: 27866/35004
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: US/09/193,043
CURRENT FILING DATE: 1993-12-23
EARLIER FILING DATE: 1993-12-23
EARLIER APPLICATION NUMBER: 08/286,889
EARLIER FILING DATE: 1994-05
EARLIER FILING DATE: 1994-12-21
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/362,652
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER APPLICATION NUMBER: 08/943,363
EARLIER PILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 114
SOPTWARE: PATENTING DATE: 2.0
SEQ ID NO 55
LENGTH: 1161
TYPE: PRT
ORGANISM: Rattus rattus
Search completed: June 13, 2005, 20:05:09 Job time : 16.9024 secs
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US-09-193-043-55
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 15.4%; Score 138.5; DB 3; Length 1161;
Local Similarity 28.3%; Pred. No. 6.7e-07;
nes 52; Conservative 36; Mismatches 71; Indels 25;
                                                                                     323 LRSI 326
                                                                                                                            165 LQGI 168
                                                                                                                                                                   267 PLEÝSDVIPAÁDKA---GIÍRÝAIGVGDAFQEPTALKELNTIGSÁPPQDHVFKVGN-FAÁ 322
                                                                                                                                                                                                    114 LFFYSE--REANRSRDLGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFFVNDGFQA 164
                                                                                                                                                                                                                                                    212 DPQSLVDPIVQLQ-----GLTYTATGIRTVMEELFHSKNGSRKSAKKILLVITDGQKYRD
                                                                                                                                                                                                                                                                                                                                    152 DIAFLIDGSGSINQRDFAQMKDFVKALMGEFASTSTLFSLMQYSNILKTHFTFTEFKNIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 LRSI 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 PLEYSDVIPAADKA---GIRYAIGVGDAPQEPTALKELNTIGSAPPQDHVFKVGN-FAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 LFFYSE--REANRSRDIGAIVYCVGVKD-FNE-TQLARI-----ADSKDHVFPVNDGFQA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTA-SVIIALTDGELHED 113
                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                    266
                                                                                                                                                                                                                                                                                                                                    211
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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B B
                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                    Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      June 13, 2005, 20:03:29 ; Search time 55.4703 Seconds (without alignments) 1195.537 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-970-076-2_COPY_44_216
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12:
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16:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*/
                                                                                                                                                                                                                                    Length DB
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jn2 6/ptcdata/1/pubpaa/US09E PUBCOMB.pep:*
jn2 6/ptcdata/1/pubpaa/US09E PUBCOMB.pep:*
jn2 6/ptcdata/1/pubpaa/US10A PUBCOMB.pep:*
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jn2 6/ptcdata/1/pubpaa/US10B PUBCOMB.pep:*
jn2 6/ptcdata/1/pubpaa/US10B PUBCOMB.pep:*
6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                            _6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
_6/ptodata/1/pubpaa/US111_PUBCOMB.pep:*
_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
            US-10-038-307-26

US-10-201-292-26

US-09-796-753-12

US-10-038-307-2

US-10-201-292-2

US-10-201-292-2

US-10-201-292-22

US-10-201-292-24

US-10-201-292-24

US-10-201-292-24

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US-10-201-292-24
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                                                                                                                                                                                                                                    Description
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Sequence
Sequence
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Sequence
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Sequence
Sequence
                                                   12, Appli 2, Appli 2, Appli 22, Appli 22, Appli 22, Appli 24, Appl
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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7.	57.7	7.	7.	.7	7.	7.	97.7	97.7	97.7	7.	97.7	97.7	97.7	9.	99.0	9	9	99.4		100.0	100.0		100.0	8	8	•	٠	8	100.0	8	8	100.0	8
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10	15	14	14	14	10	14	14	14	14	14	14	14	14	16	16	10	10	H	16	16	16	14	14	14	10	10	14	14	13	14	14	14	14
-09-796-753-54	- 1	-10-368-087-1	-10-201-292-	-10-038-307-	-09-796-753-	-10-201-2	-10-201-292-1	-10-201-292-	-10-038-307-	-10-038-307-1	-10-038-307-1	-10-201-29	-10-038-	-10-474-794-	US-10-474-794-194	-09-918-715-	-09-918-715-	-09-833-245-	-10-474-794-	-10-474-794-	-10-408-765A	0-301-822-	US-10-201-292-20	-10-038-307-	-09-918-715-	-09-918-715-18	0-201-292-1	-10-038-307-1	-10-047-542-	-10-201-292-3	-201-292-3	-10-201-292-3	01-292-
equence 54,	263	equence 16,	е 6,	equence 6,	e 52,	equence 16,	14,	equence 10,	16,	equence 14,	10,		e 12,	e 301	e 194	e 301	194	e 620	232		1823	199,	20,	20,	e 232,	e 187,	e 18,	e 18,	equence	equence 36,	e 34,	equence 32,	Sequence 30, Appl

ALIGNMENTS

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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNK;
APPLICANT: Engin OZKAYNK;
APPLICANT: Loudith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION UNDER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-307-26
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                                                                                                                                                                                                                                                                Query Match 100.0%; Score 899; DB 1
Best Local Similarity 100.0%; Pred. No. 1e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/10038307
Publication No. US20030134786A1
                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                               104
                                                                                                                                                                                                                                    173;
121 EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 173
                                                                                               61 QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER 120
                                                                                                                                               44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR 103
                                                                                                                                                                             1 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR 60
                                               QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                         <u>,</u>
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                                                                                                                                                                                                                                                                                         DB 14; Length 328;
                                                                                                                                                                                                                                            Indels
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                                                                                                                                        CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,
PRIOR FILLING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,
PRIOR FILLING DATE: 1998-12-30
PRIOR FILLING DATE: 1998-12-30
PRIOR FILLING DATE: 1998-12-30
PRIOR PRIOR PAPELICATION NUMBER: 09/224,
PRIOR APPLICATION NUMBER: 09/224,
PRIOR APPLICATION NUMBER: 09/259,
PRIOR APPLICATION NUMBER: 09/259,
PRIOR APPLICATION NUMBER: 60/122,
PRIOR APPLICATION NUMBER: 09/312,
PRIOR APPLICATION NUMBER: 09/312,
PRIOR APPLICATION NUMBER: 09/312,
PRIOR APPLICATION NUMBER: 09/312,
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PRIOR APPLICATION NUMBER: 09/312,
PRIOR APPLICATION NUMBER: 09/312,
PRIOR APPLICATION NUMBER: 09/312,
PRIOR APPLICATION NUMBER: 09/312,
PRIOR FILING DATE: 1999-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEO ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 173; Conservat
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
APPLICATION NUMBER: 09/
FILING DATE: 1999-06-30
APPLICATION NUMBER: 09/
                                                                                                 APPLICATION NUMBER:
                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
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VENTION: SECRETED PROTEINS AND USES THEREOF
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vo. US20030144193A1
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                                                                          1999-06-29
                                                                                                                           1999-06-18
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100.0%; Pred. No. 1e-86;
tive 0; Mismatches 0;
                                                   09/345,464
                                                                                                                                                                                                                                                                                                   09/259,388
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                                                                                                                                                                                                                                                                                                                                                                                                  09/223,546
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                                                                                                                                                  09/336,536
                                                                                                    09/342,687
                                                                                                                                                                                                   09/312,359
                                                                                                                                                                                                                                                    60/122,458
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                                                                                                                                                                                                                                                                   US-10-038-307-2
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                Sequence 2, Application US/10038307
Publication No. US20030134786A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 20
NUMBER OF SEQ ID NOS:
SEQ ID NO 12
LENGTH: 333
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Best Local (
                                                                                                              APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
                                                                                                                                                                                   APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-09-20 PRIOR APPLICATION NUMBER: 09/
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FILING DATE: 1999-12-23
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                                                                                                                                                                                                                                                                                                                                  164 EANRSRDIGATVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 216
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RESULT 6
US-10-038-307-22
Sequence 22, Application US/10038307
Sequence 22, Application US/10038307
Publication No. US20030134788A1
GENERAL INFORMATION:
APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/038,307
CURRENT APPLICATION UNMBER: US/10/038,307
CURRENT APPLICATION USBER: US/10/038,307
CURRENT FILING DATE: 2002-06-28
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APPLICANT: Theresa L. O'KEEFE
APPLICANT: Engin OZKAYNAK
APPLICANT: LOUGITH J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-038-307-2
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Windows Version 4.0
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; SEQ ID NO 22
; LENGTH: 342
; TYPE: PRT
; TYPE: PRT
; ORCANISM: Homo sapiens
US-10-038-307-22
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; ORGANISM: Homo
US-10-201-292-22
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                 Sequence 24, Application US/10038307

Publication No. US20030134786A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTMAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

ITTLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods

FILE REFERENCE: 7853-253-999
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 342
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Best Local Similarity
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APPLICANT: Theresa L. O'KESPE
APPLICANT: Engin OZKAYNAK
APPLICANT: Undith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions
FILE REFERENCE: 7863-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
CURRENT APPLICATION NUMBER: US/10/038,307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Sequence 24, Application US/10201292

Publication No. US20030144193A1

GENERAL INFORMATION:

APPLICANT: James B. ROTTWAN

APPLICANT: Theresa L. O'KEEFE

APPLICANT: Engin OZKAYNAK

APPLICANT: Judith J. HEALEY

TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and

FILE REFERENCE: 7853-253-999

CURRENT APPLICATION UNMBER: US/10/201,292

CURRENT FILING DATE: 2003-02-14

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 345
                                                                                                                                       RESULT 10
US-09-833-245-621
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            Sequence 621, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
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Matches
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NUMBER OF SEQ ID NOS: 26
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 24
LENGTH: 345
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CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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NUMBER: US/09/833,245
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PRIOR APPLICATION NUMBER: 60/229, 31
PRIOR FILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-12-56, 91
PRIOR FILING DATE: 2000-12-21
PRIOR PILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 36
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 621
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APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 460
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Best Local Similarity
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Publication No.
                                                                                                                                                                                                                Matches 173;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: James B. ROTTMAN
                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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164
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                                                                                         61 QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER 120
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                                                                                                                                       44 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
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                  EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 173
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                                                                    QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Theresa L. O'KEEFE
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No. US20030144193A1
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Pred. No. 1.6e-86;
D; Mismatches 0;
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Pred. No. 1.4e-86;
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RESULT 12 US-10-201-292-30

Sequence 30,

Application US/10201292

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APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEPE
APPLICANT: Engin OZKAYNAK
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
ITITE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-2959
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT APPLICATION UNDER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-201-292-32
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CURRENT FILING DATE: 2003-02-14
NUMBER OF BEG ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 479
                                                                                                                                                                                                                                                                                     Matches 173;
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                                                                                                                                                                                                                                                                                                             Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KEEPE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
FILE REFERENCE: 7853-253-999
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                              121
                                                                                          104 QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 EANRERDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSIL 216
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                                                                                                                        61 QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER 120
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                                                                                                                                                                                                                                                                                                             Similarity
EANRSRDIGATVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL 216
                             EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSIL 173
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                                                                                                                                                                                                                                                                                100.0%; Score 899; DB 14; 100.0%; Pred. No. 1.7e-86; tive 0; Mismatches 0;
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US-10-201-292-36
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; ORGANISM: Homo sapiens
US-10-201-292-36
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US-10-201-292-34
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US-10-201-292-34
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 504
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/10201292 Publication No. US20030144193A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34, Application US/10201292 Publication No. US20030144193A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                     Matches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: James B. ROTTMAN
APPLICANT: Theresa L. O'KESEE
APPLICANT: Engin OZKAYNAK
APPLICANT: Judith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and Methods
FILE REFERENCE: 7853-253-999
CURRENT APPLICATION NUMBER: US/10/201,292
CURRENT FILING DATE: 2003-02-14
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APPLICANT: Thereea L. O'KREFE
APPLICANT: Engin OZKAYNAK
APPLICANT: Uddith J. HEALEY
TITLE OF INVENTION: Tango 197 and Tango 216 Compositions and
FILE REFERENCE: 7853-253-999
FILE REFERENCE: 7853-253-999
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                                                                                                  61
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EANRSRDLGAIVYCVGVKDENETQLARIADSKDHVFPVNDGFQALQGIIHSIL 173
                                                                                  QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER 120
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                                                             QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
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Pred. No. 2e-86;
Mismatches
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Listing first 45
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seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                             DLYFILDKSGSVLHHWNEIY......
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Pred. No. score grea and is der No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	v	4	w	N		Result
87		87.5	88	88	88	88.5	91.5	92.5	93		98.5	99	100	100.5	101.5	102	104.5	109	110	110	110	113.5	120.5	121.5	121.5	125	120.5	129.5	Score
9.7			9.8			9.8				10.7			11.1				•	12.1	•		12.2		13.4		13.5	13.9	14.3	14.4	Query Match
710	418	341	1218	1018	917	932	1179	3137	3176	761	1029	698	460	567	764	2944	929	3051	1888	1857	1747	760	1153	1163	712	3124	1153	724	Length
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hypothetical prote		hypothetical prote	valine-tRNA ligase	alpha	collagen alpha 2(V	pha-inhib	alpha-E		21	complement factor	⋾			hypothetical prote	complement factor	collagen alpha 1(V	co11	al pro	collagen alpha 1(X	collagen alpha 1(X	collagen alpha 1(X	classical-compleme	leukocyte surface	cell surface glyco	immunodominant mic		cell surface glyco	antigen Em100 - Ei	cription

ALIGNMENTS

C; Accession: A48569

;Species: Eimeria maxima ;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

to the Eimeria tenella mi

antigen Em100 -

Eimeria maxima

```
cell surface glycoprotein CD11b precursor [validated] - human
N;Alternate names: complement receptor type 3 alpha chain; leukocyte adhesion protein Ma
eukocyte integrin alpha chain; neutrophil adherence receptor alpham chain
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text change 09-Jul-2004
C;Accession: A31108; A28915; A41600; A30892; A32218; A46526; A26091; I52567
R;Corbi, A.L.; Kishimoto, T.K.; Miller, L.J.; Springer, T.A.
J. Biol. Chem. 263, 12403-12411, 1988
A;Title: The human leukocyte adhesion glycoprotein Mac-1 (complement receptor type 3, CD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q04588; GB:M99058; NID:g158890; PID:g158891
A;Note: sequence extracted from NCBI backbone (NCBIN:123776, NCBIP:123777)
F;45-218/Domain: von Willebrand factor type A repeat homology <VWA2>
F;238-296/Domain: thrombospondin type 1 repeat homology <THR1>
F;309-371/Domain: thrombospondin type 1 repeat homology <THR3>
F;372-432/Domain: thrombospondin type 1 repeat homology <THR3>
F;433-493/Domain: thrombospondin type 1 repeat homology <THR3>
F;433-493/Domain: thrombospondin type 1 repeat homology <THR5>
F;494-556/Domain: thrombospondin type 1 repeat homology <THR5>
F;560-610/Domain: thrombospondin type 1 repeat homology <THR6>
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A;Title: Sequence of a major Bimeria maxima antigen homologous A;Reference number: A48569; MUID:93149203; PMID:8426611
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A; Residues: 1-724 < PAS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 LFFYSERE-----ANRSRDLGAIVYCVGV-KDFNETQLARIA--DSKDHV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 QIRQGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGYR--TASVIIALTDGELHED 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QNADLLAAAAKKLPYAAGSTYTHLGLAKA-EEILFSFQKGGRDNAPKMILVMTDGA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SSRRSQTLSAAEKLRNRGVIIVVLGVGTGVNSAECRSIAGCDTSDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
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A; Molecule type: mRNA
A; Residues: 9-1153 <HIC>
A; Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Cross-references: GB:J04145; NID:g189068; PIDN:AAA59903.1; PID:g386975
A; Mote: part of this sequence was confirmed by protein sequencing
R; Fleming, J.C.; Pahl, H.L.; Gonzalez, D.A.; Smith, T.F.; Tenen, D.G.
J. Immunol. 150, 480-490, 1993
A; Title: Structural analysis of the CD11b gene and phylogenetic analysis of tl
n during evolution.
A; Reference number: A46526; MUID:93123748; PMID:8419480
A; Reference number: A46526
A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-499,501-1153 <FIE>
A; Cross-references: GB:S52227; NID:g263047; PIDN:AAB24821.1; PID:g263049
A; Note: the last three bases of intron 13, CAG, are included in some but not in the sequence extracted from NCBI backbone (NCBIP:121963)
A; Pierce, M.W.; Remold-O'Donnell, E.; Todd III, R.F.; Arnaout, M.A.
Biophys. Acta 874, 368-371, 1986
A; Title: N-terminal sequence of human leukocyte glycoprotein Mo1: conservation
A; Accession: A26091
A; Accession: A26091
A; Molecule type: Did ackbone of human leukocyte glycoprotein Mo1: conservation
A; Accession: A26091
                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 17-31 <PIE>
A; Residues: 17-31 <PIE>
A; Experimental source: granulocytes
R; Pahl, H.L.; Rosmarin, A.G.; Tenen, D.G.
Blood 79, 865-870, 1992
Blood 79, 865-870, 1992
A; Title: Characterization of the myeloid-specific CD11b
A; Reference number: I52567; MUID: 92144986; PMID: 1346576
A; Accession: I52567
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R;Hickstein, D.D.; Hickey, M.J.; Ozols, J.; Baker, D.M.; Back, A.L.; Roth, Proc. Natl. Acad. Sci. U.S.A. 86, 257-261, 1989
A;Title: CDNA sequence foor the alpham subunit of the human neutrophil adher A;Reference number: A32218; MUID:89098893; PMID:2563162
A;Accession: A32218
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Proc. Natl. Acad. Sci. U.S.A. 88, 10525-10529, 1991
A;Title: The promoter of the CD11b gene directs myeloid-specific and developmentally A;Reference number: A41600; MUID:92073318; PMID:1683702
A;Accession: A41600
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A; Residues: 1-499,501-965,'p',967-1153 <ARN>
A; Residues: 1-499,501-965,'p',967-1153 <ARN>
A; Crose-references: GB: M18044; GB: J03270; GB: M19664; GB: X07421; NID: g186935; PIDN: AAA59.
A; Note: the authors translated the codon TAC for residue 1129 as Thr
A; Note: part of this sequence, including the amino end of the mature protein, was confined the codon.
C;Genetics:
                           A;Cross-references: GB:MC;Comment: A common beta
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A;Note: part of this sequence was confirmed by protein sequencing
A;Arnaut, M.A.; Guta, S.K.; Pierce, M.W.; Tenen, D.G.
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A; Residues: 1-1153 < COR>
                                                                                                           A;Residues: 1-9 <RES>
                                                                                                                                               A;Molecule type:
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A;Residues: 917-1042 <AR2>
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A; Residues: 1-9 <SHE>
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cl. 106, 2153-2158,
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                           GB:M84477; NID:g180184; PIDN:AAA51960.1; PID:g553219 beta chain (CD18) forms a heterodimer with this chai
                                                                                                                                                                                       GB/EMBL/DDBJ
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P.; Tenen,
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A;Accession: B34485
A;Molecule type: protein
A;Residues: 2772-2792;2846-2873 <GOR2>
A;Residues: 2772-2792;2846-2873 <GOR2>
R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA
A;Reference number: A28037; MUID:87317590; PMID:3476925
A;Accession: A28037
A;Molecule type: mRNA
A;Residues: 2960-2976,'F',2978-3074,'AG' <GOR3>
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A;Residues: 1-3124 <YAM'>
A;Residues: 1-3124 <YAM'>
A;Residues: 1-3124 <YAM'>
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A;Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:g222811
A;Cross-references: UNIPROT:P13944; GB:D00824; NID:g222810; PIDN:BAA00701.1; PID:g222811
A;Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.
J. Biol. Chem. 264, 19772-19778, 1999
A;Title: Type XII collagen. A large multidomain molecule with partial homology to type II
A;Reference number: A34485; MUID:90062079; PMID:2584192
A;Accession: A34485
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revi
C;Accession: A40020; #34485; B34485
C;Accession: A40020; #34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485; B34485
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A;Note: product.

A;Note: product.

A;Note: product.

A;Note: product.

C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A repeat homol C;Superfamily: cell surface glycoprotein; cell adhesion; glycoprotein; heterodimer; magr F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-1153/Product: cell surface glycoprotein CD11b #status experimental <MAT>
F;17-109/Domain: extracellular #status predicted <EXT'>
F;148-318/Domain: von Willebrand factor type A repeat homology <VWA2>
F;465-473/Region: calcium/magnesium binding #status predicted F;533-601/Region: calcium/magnesium binding #status predicted F;1109-1134/Domain: transmembrane #status predicted <TMM>
F;1135-1153/Domain: intracellular #status predicted <INT>
F;186,240,391,469,693,697,735,802,881,901,912,941,947,979,994,1022,1045,1051,1076/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: EMBL:J05137; NID:g211284; PIDN:AAA48635.1; PID:g211285
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A;Accession: A40020
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A;Cross-references: GDB:120599; OMIM:120980
A;Map position: 16p11.2-16p11.2
A;Note: promoter contains a GATA motif and i
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sion: A40020; A34465; B34485; A28037; S23814; S22254; S28811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGEKFGDPLGYEDVIPEADRE----GVIRYVIGVGDAFRSEKSRQELNTIÅSKPPRDHVFQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGELHEDLFFYSE--REANRSRDLGAIVYCVGVKDFNETQLAR----IADS--KDHVFP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.3%;
ilarity 26.7%;
Conservative 3
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Pred. No. 0.0042;
B; Mismatches 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.S.; Shinomura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T.; Tanaka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H.; Nishida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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F/24-114/Domain: IIIA #status predicted <111A>
F/24-105/Domain: fibronectin type III repeat homology <FN3A>
F/24-105/Domain: fibronectin type III repeat homology <VWA1>
F/32-30/Domain: IIIB #status predicted <IIIB>
F/332-445/Domain: fibronectin type III repeat homology <FN3B>
F/332-414/Domain: fibronectin type III repeat homology <FN3C>
F/332-1178/Domain: IIIC #status predicted <IIIC>
F/630-1178/Domain: fibronectin type III repeat homology <FN3C>
F/30-711/Domain: fibronectin type III repeat homology <FN3D>
F/812-895/Domain: fibronectin type III repeat homology <FN3E>
F/905-986/Domain: fibronectin type III repeat homology <FN3F>
F/905-1076/Domain: fibronectin type III repeat homology <FN3G>
F/1086-1169/Domain: fibronectin type III repeat homology <FN3H>
F/1086-1169/Domain: fibronectin type III repeat homology <FN3H>
F/1197-1361/Domain: fibronectin type III repeat homology <FN3H>
F/1197-1361/Domain: fibronectin type III repeat homology <FN3H>
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F;1384-1465/Domain: fibronectin type III repeat homology <FN3I>
F;1474-1557/Domain: fibronectin type III repeat homology <FN3J>
F;14674-1557/Domain: fibronectin type III repeat homology <FN3J>
F;1566-1647/Domain: fibronectin type III repeat homology <FN3N-
F;1655-1738/Domain: fibronectin type III repeat homology <FN3N-
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F;1897-2019/Domain: fibronectin type III repeat homology <FN3N-
F;1897-2019/Domain: fibronectin type III repeat homology <FN3P-
F;2028-2110/Domain: fibronectin type III repeat homology <FN3P-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3P-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3P-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3P-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3P-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294/Domain: fibronectin type III repeat homology <FN3R-
F;2017-2294
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A;Title: Type XII collagen is expressed in
A;Reference number: S22254; MUID:88087065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Biochem. 207, 847-856, 1992
A;Title: A major oligomeric fibroblast proteoglycan identified A;Reference number: S23814; MUID:92362621; PMID:1323460
A;Accession: S23814
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A,Residues: 1-24,1189-1257,'8',1259-1263,'E',1265-1280
A,Cross-references: EMBL:X67327
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A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517
R;Dublet, B.; van der Rest, M.
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                                                                                                                                                                                                                                                                                                                                                              F;2903-2945/Domain: non-collagenous NC2 #status predicted <NC2>F;2946-3048/Domain: collagenous COL1 #status predicted <COL1>F;3946-3124/Domain: non-collagenous NC1 #status predicted <NC1>F;3049-3124/Domain: non-collagenous NC1 #status predicted <NC1>F;32,1006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site:
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A,Title: The two splice variants of collagen XII share a common
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A;Residues: 2831-2832,'T',2834,'R',2836-2843;3002-3014 <DUB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;2325-2490/Domain: von Willebrand factor type A repeat homology <VWA4>;2438-2440/Region: cell adhesion #status predicted;2509-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status predicted;2751-2902/Domain: collagenous COL2 #status predicted <COL2>;2509-2901/Region: cell attachment (R-G-D) motif
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                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                             006,1032,1044,1512,1767,2210,2273,2532,2683/Binding site: carbohydrate,2789,2836,2842,2860,2866,2869,3004,3007/Modified site: hydroxyproline
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                                                                                                                                                                                           Similarity
DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF--ISPQ-LRMSFIVFSTRGTTLMKLT--E 54
                                                                                                                                                Conservative
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splicing; cell binding; coiled coil; connective t
                                                                                                                                                                                 13.9%; Score 125; DB 2
27.1%; Pred. No. 0.028;
                                                                                                                                                39; Mismatches
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PMID:3121603
                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                 Length 3124;
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1163 <COR>
A; Cross-references: UNIPROT: P20702
A; Cross-reference this revision to the sequence from reference A35543 includes
A; Note: this revision to the sequence from reference A35543 includes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;238-296/Domain: thrombospondin type 1 repeat homology <THR1> F;309-371/Domain: thrombospondin type 1 repeat homology <THR2> F;309-371/Domain: thrombospondin type 1 repeat homology <THR3> F;372-432/Domain: thrombospondin type 1 repeat homology <THR4> F;433-493/Domain: thrombospondin type 1 repeat homology <THR4> F;494-556/Domain: thrombospondin type 1 repeat homology <THR5> F;560-610/Domain: thrombospondin type 1 repeat homology <THR6>
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A;Title: Sequence of the gene encoding an immunodominant microneme A;Reference number: A45638; MUID:92131064; PMID:1775171
A;Accession: A45638
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A45638
R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A.
J. Biol. Chem. 265, 2782-2788, 1990
A;Tille: Genomic structure of an integrin alpha subunit,
A;Reference number: A35543; MUID:90153906; PMID:2303426
                                                                                                                                                                                                                                                                                                                                                        R;Corbi, A.L.; Garcia-Aguilar, J.; Springer, T.A. J. Biol. Chem. 265, 12750-12751, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:043981; GB:AF032905; GB:M73495; NID:g2707732; A;Note: sequence extracted from NCBI backbone (NCBIN:77752, NCBIP:77756) F;48-218/Domain: von Willebrand factor type A repeat homology <VWA1>
                                                                                                                                                                                                                                                                                     A; Reference number: A36584
A; Contents: erratum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: leukocyte adhesion receptor p150,95 alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell surface glycoprotein CD11c precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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C;Species: Eimeria tenella
C;Jate: 22-Apr-1993 #sequence_revision 18-Nov-1994
                                                                                                                                                                                                                                                                                                                                                                                                             ;Species: Homo sapiens (man)
;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
;Accession: A35584; A35543; S00864
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                                                                                                                                                                                                                                                             Accession: A36584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVMTDGA--SNLPSQTRSSAAALRDAGAIVVVLGVGSGVNSSECRSIA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IALTDGELHEDLFFYSEREANRSRDLGAIVYCVGV-KDFNETQLARIA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIRQGLEELQKVLPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF-ISPQ-LRMSFIVFSTRGTTLMKLTEDRE 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVRWNLSDPKATNPSLAISAARSLSYSTGVTYTHYGLQDA-KKLLYDTNAGARNNVPKLV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVMLVVDESGSIGTSNFRKVRQFIEDFVNSMPISPEDVRVGLITFAT------RS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DREQIRQGLEELQKVLPGGDTYMHEGFERASEQIY-YENRQGYRTASVIIALTDGELHED 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 121.5; DB Pred. No. 0.0097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDTYMHEGFERASEQIYYENRQGYR--TASVI 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
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                                        the
                                        leukocyte
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                                                                                                                                     the carboxyl
                                        p150,95 molecule
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A;Gene: Mac-1 C;Superfam:

factor type A repeat homo.

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A;Molecule type: DNA
A;Residues: 1-1153 <PYT>
A;Residues: 1-1153 <PYT>
A;Residues: 1-1153 <PYT>
A;Residues: references: UNIPROT:P0555; EMBL:X07640; NID:g52982; PIDN:CAA30479.1; PID:g52983
A;Note: the authors translated the codon CAC for residue 569 as Gln
R;Sastre, L.; Roman, J.M.; Teplow, D.B.; Dreyer, W.J.; Gee, C.E.; Larson, R.S.; Roberts, Proc. Natl. Acad. Sci. U.S.A. 83, 5644-5648, 1986
A;Title: A partial genomic DNA clone for the alpha subunit of the mouse complement recept A;Reference number: I59078; MUID:86287312; PMID:2942940
A;Accession: I59078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukocyte surface glycoprotein Mac-1 alpha chain precursor - NyAlternate names: complement-3 receptor alpha chain C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1999 #sequence_revision 30-Sep-1991 #text_char C;Accession: S00551; I59078
R;Pytcla, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: calcium; cell adhesion; glycoprotein; heterodimer; magnesium; tandem reper; 1-19/Domain signal sequence #status predicted <SIG>
F;20-1163/Product: cell surface glycoprotein CDII: #status predicted <MAT>
F;20-1107/Domain: extracellular #status predicted <EXT>
F;149-319/Domain: von Willebrand factor type A repeat homology <VWAA>
F;1108-1133/Domain: transmembrane #status predicted <INT>
F;1134-1163/Domain: intracellular #status predicted <INT>
F;1134-1163/Domain: intracellular #status predicted <INT>
F;61,89,392,697,735,899,939,1050/Binding site: carbohydrate (Asn) (covalent) #status
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A;Molecule type: mRNA
A;Residues: 1-755,'L',757-1163 <CO3>
A;Residues: 1-755,'L',757-1163 <CO3>
A;Residues: 1-755,'L',757-1163 <CO3>
A;Residues: part of this sequence was confirmed by protein sequencing
A;Note: part of this sequence was confirmed by protein sequencing
A;Note: part of this sequence was confirmed by protein sequencing
A;Note: part of this sequence was confirmed by protein sequencing
A;Note: part of this sequence was confirmed by protein sequencing
A;Note: part of this sequence was confirmed by protein sequencing
A; Cross-references:
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A; Map position: 16p11.2-16p11.2
C; Superfamily: cell surface glycoprotein CD11b; von Willebrand
C; Superfamily: cell surface glycoprotein; heterodimer;
                                   A; Molecule type: DNA
A; Residues: 11-44 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S00551;
A; Accession: S00551
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                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLDYKD-VIPMADAAGIIRYAIGVGLAFQNRNSWKELND----IASKPSQEHIFKVED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPLSLLASVHQLQ-----GFTYTATAIQNVVHRLFHASYGARRDATKILIVITDGKKEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDRE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---QIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTAS-VIIALTDGELHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIVFLIDGSGSISSRNFATMMNFVRAVISQFQRPSTQFSLMQFSNKFQTHFTFEEFRRTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
   GB:M14293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       e of the murine MUID:88312584;
NID:g198993; PIDN:AAA39484.1; PID:g554193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMIM: 151510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 121.5; DB Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-Sep-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in reference A36584
K.; Larson, R.S.; Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mac-1 alpha chain
PMID:3044779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   structure of the alpha subunit PMID:3327687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reveals homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      magnesium; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
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A;Molecule type: mRNA
A;Rolecule type: mRNA
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A;Introne: 16/1; 91/1; 153/1; 212/1; 245/3; 290/3; 337/1; 384/1; 414/1; 461/1
C;Complex: The proenzyme forms a complex with C4a and is activated by cleavag
C;Function:
C;Complex: The proenzyme forms a complement C3 and complement C5 alpha chains
A;Description: cleaves complement C3 and complement C5 alpha chains
A;Description: cleaves complement C3 and complement Factor H repeat homology; trypsin
C;Keywords: alternative splicing; complement classical pathway; duplication;
F;13-280/Droduct: complement C2b fragment #status predicted <C2B>
F;13-280/Domain: complement factor H repeat homology <FH1>
F;24-819/Domain: complement factor H repeat homology <FH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-760 <182>
A;Cross-references: UNIPROT:P21180; GB:M57891; GB:J05661; NID:g192436; PIDN:AAA63294.1;
A;Cross-references: UNIPROT:P21180; GB:M57891; GB:J05661; NID:g192436; PIDN:AAA63294.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: I54429
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Falus, A.; Wakeland, E.K.; McConnell, T.J.; Gitlin, J.; Immunogenetics 25, 290-298, 1987
A;Ttle: DNA polymorphism of MtC III genes in inbred and A;Reference number: I54429; MUID:87192938; PMID:2883115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-760 <ISH>
A;Residues: 1-760 <ISH>
A;Cross-references: EMBL.M57891; NID:g192436; PIDN:AAA63294.1; PID:g192437
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A;Cross-references: EMBL.M57891; NID:g192436; PIDN:AAA63294.1; PID:g192437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Murine complement C
A;Reference number: A36593;
A;Accession: B36593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Ishikawa, N.; Nonaka, M.; Wetsel, J. Biol. Chem. 265, 19040-19046, 19A;Title: Murine complement C2 and f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993
C;Accession: A38876; B36593; T54429
R;Ishikawa, N.; Nonaka, M.; Wetsel, R.A.; Colten, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: cell surface glycoprotein CD11b; von Willebrand factor type A C;Keywords: cell adhesion; glycoprotein; transmembrane protein F;1-16,Domain: signal sequence #status predicted <SIG> F;17-1153/Product: leukocyte surface glycoprotein Mac-1 alpha chain #status F;148-318/Domain: von Willebrand factor type A repeat homology <VWA2> F;1106-1129/Domain: transmembrane #status predicted <TWM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to GenBank, January 1991
A;Reference number: A38875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A38876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           classical-complement-pathway C3/C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 VNDGFQALQGI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               names: C3 convertage; C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DLYFILDKSGSVLHHWNEIYYFVEQLAHKFIS---PQLRMSFIVFSTRGTTLMKLTED--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V-DNFEALNTI 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGEKFGDPLDYKDVIPEADRA---GVIRYVIGVGNAFNKPQSRRELDTIASKPAGEHVFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%; Score 120.5; DB 27.2%; Pred. No. 0.021; tive 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2 and factor B MUID:91035430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           convertase (EC 3.4.21.43)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               convertase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic and
PMID:2229060
                                                                                                                                                                                                                                                                       290/3; 337/1; 384/1; 414/1; 461/1; th C4a and is activated by cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse strains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.S.; Colten,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                        homology; voglycoproteir
                                                                                                                                                                                                                                                                       492/3; 53; into C2a,
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N;Alternate names: undulin
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974; 830085; 822916; 817035; 820833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, J. Biol. Chem. 268, 12177-12184, 1993
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P;251-760/Product: complement C2a fragment long form #status predicted <C2A>
P;251-605,613-760/Product: complement C2a fragment short form #status predicted <C2S>
P;259-449/Domain: von Willebrand factor type A repeat homology <VFA>
P;478-747/Domain: trypsin homology #status atypical <TRY>
P;22-62,49-98,94-136,122-149,156-197,182-210,470-590,499-515,593-609,647-674,685-715/Dis
P;27-62,49-98,94-136,122-149,156-197,182-210,470-590,499-515,593-609,647-674,685-715/Dis
P;27,117,297,340,474,478,663/Binding site: carbohydrate (Asn) (covalent) #status predicted
P;514,570,689/Active site: His, Asp, Ser #status predicted
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A;Residues: 286-494,'Q, 496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU>
A;Residues: 286-494,'Q, 496-834,'A',836-1119,'KL',1122-1402,1409-1439 <TRU>
R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der Rest, M.; Mayne,
Eur. J. Blochem. 201, 333-338, 1991
Eur. J. Blochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens
A;Reference number: S17035; MUID:92037585; PMID:1935930
                                                                                                                                                                                                                                                                                                                                                                                   R;Trueb, J.; Trueb, B.
Eur. J. Biochem. 207, 549-557, 1992
Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of A;Reference number: S22916; MUID:92339443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data A/Reference number: S30085 A/Accession: S30085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: sequence R;Apte, S.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Experimental source: embryo skin A, Note: sequence inconsistent with the nucleotide translation A, Note: sequence extracted from NCBI backbone (NCBIN:133364, )
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A; Residues: 1472-1660 < APT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A45974; MUID:93280195; A;Accession: A45974
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A,Molecule type: mRNA
A,Residues: 1472-1659 <GORl>
                                                                     A; Accession: S17035
                                                                                                                                                                                                                                                                                                                A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                     A, Accession: S22916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X65122; NID:g62871; PIDN:CAA46238.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Cross-references: UNIPROT: P32018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Title: Type XIV collagen is encoded by alternative transcripts with distinct 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen alpha 1(XIV) chain precursor, short form
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PMID:1339349
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A; Molecule to A; Residues: C; Keywords: F; 40-204/Dom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-1857 <WAE>
A;Cross-references: EMBL:X70792; NID:g288874;
A;Cross-references: EMBL:X70792; NID:g288874;
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;Reywords: alternative splicing; coiled coil.
;Reywords: alternative splicing; coiled coil.
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;Reywords: alternative splicing; coiled coil.
;Repeat homology < rN3A>
;Reysologies of the coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled coiled 
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F;29-1857/Product: collagen alpha 1(XIV) chain, short form #status predicted F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
F;156-320/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3C>
F;444-525/Domain: fibronectin type III repeat homology <FN3C>
F;447-525/Domain: fibronectin type III repeat homology <FN3D>
F;534-614/Domain: fibronectin type III repeat homology <FN3B>
F;633-707/Domain: fibronectin type III repeat homology <FN3F>
F;741-823/Domain: fibronectin type III repeat homology <FN3G>
F;833-914/Domain: fibronectin type III repeat homology <FN3G>
F;833-914/Domain: fibronectin type III repeat homology <FN3G>
F;833-914/Domain: fibronectin type III repeat homology <FN3G>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown; translation not
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les 48; Conserv
     1042 DLVFLVDGSWSIGDDNFNKIISFLYSTVGALDKIGPDGTQVAIIQFSDDPRTEFKLNAYK 110:
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                                                                                                                                                                                                   48;
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                                                                                                                                                                                                                                             Similarity
                                                                                            DLYFILDKSGSV-LHHWNEIYYFVEQL--AHKFISPQ-LRMSFIVFSTRGTTLMKLT--E 54
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                                                                                                                                                                                                                                                                                                                                                                                             fibronectin type von Willebrand
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                                                                                                                                                                                         Score 110; DB:
Pred. No. 0.3;
37; Mismatches
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Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                                                                                                                  factor
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                                                                                                                                                                                                                                                                                                                                                                                             type
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                                                                                                                                                                                                                                                                                                                                                                                        homology
A repeat
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A;Gene: Col14A1

C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycopr:
F;1-28/Domain: signal sequence #status predicted <SIG>
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1888/Product: collagen alpha I(XIV) chain, long form #status predicted .
F;29-10/Domain: fibronectin type III repeat homology <FW3B>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
F;352-433/Domain: fibronectin type III repeat homology <FW3B>
F;442-525/Domain: fibronectin type III repeat homology <FW3B>
F;534-614/Domain: fibronectin type III repeat homology <FW3B>
F;623-707/Domain: fibronectin type III repeat homology <FW3B>
F;741-823/Domain: fibronectin type III repeat homology <FW3B>
F;741-823/Domain: fibronectin type III repeat homology <FW3B>
F;741-823/Domain: fibronectin type III repeat homology <FW3B>
F;922-1009/Domain: fibronectin type III repeat homology <FW3B>
F;922-1009/Domain: fibronectin type III repeat homology <FW3B>
F;1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>
                                              hypothetical protein T20G5.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;pate: 07-Oct-1994 #sequence_revision 10-Nov-1995 #t/C;Accession: S42373 R;Smith, A.
A; Reference number:
                                                                                                                                                                                   RESULT 11
S42373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-1888 <TRU>
A;Cross-references: UNIPROT:P32018; EMBL:X70793; NID:g288872
A;Cross-references: UNIPROT:P32018; EMBL:X70793; NID:g288872
R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.;
Eur. J. Biochem. 212, 483-490, 193
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
A;Accession: S31211
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A;Residues: 1-416;1460-1811,1843-1888
A;Crose-references: EMBL:X70793
C;Genetics:
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submitted to the EMBL Data A; Reference number: S42368
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                           March 1994
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                                                                                               10-Nov-1995 #text_change 09-May-2004
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type XII collagen alpha-1 chain - eastern newt (fragment) (C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-20 C;Accession: I51027
N;Alternate names: procollagen alpha 1(VII) chain C;Species: Homo sapiens (man) C;Cpecies: Homo sapiens (man) C;Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text_change C;Accession: A54849; PH0844; S16316; I56328; A30296; I84686
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I51027
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F;631-795/Domain: von Willebrand fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Monoclonal antibody MT2 identifies the urodele alpha A;Reference number: I51027; MUID:95246925; PMID:7729585
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                                                                                                collagen alpha 1 (VII) chain precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q91145; EMBL:U19494; NID:g632647; PIDN:AAA80217.1; PID:g63264
F;155-236/Domain: fibronectin type III repeat homology <3FR>
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A; Residues: 1-929 <WEI>
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Dev. Biol. 168, 503-513,
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A; Molecule type: DN
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                                                                                                                                                                                                                                                                                                                               693 KKSLMDAVANLPYKGGNTNTGSALKFILENNF---RPGVGMREKARKIAILLTDGKSQDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                514 DLVFLIDGSGSIGSYVFKNEVLRFVREFVELFEIGRSKTRVGLIQYSDQIRHEFDLDQYG 573
                                                                                                                                                                                                                                                                                                                                                                              60 ROGLEELQKVLP--GGDTYMHEGFERASEQIYYENRQGY----RTASVIIALTDGELHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 DREQIRQGLEELQKVLPG----GDTYMH---EGFERASEQIYYENRQGYR-----TASVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DLYFILDKSGSV-LHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQALQGIIHSIL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRDSLLKGISETQ-YLTGLTRTGAAIQHMVQEGF-----SERRGARPQQSDIARVA 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IILTDGRSQDNV----TGPADSARKLSINTFAIGVTDHVLASELESIAGSPNRWFYY-DK 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.6%; Score 104.5; I 23.3%; Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 109; DB
Pred. No. 0.67
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor type A repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74;
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                            09-Jul-2004
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A;Molecule type: mRNA
A;Residues: 'RFR',372-517,'DV',520-540,'W',542-1255 <RES>
A;Residues: 'RFR',372-517,'DV',520-540,'W',542-1255 <RES>
A;Cross-references: GB:551236; NID:g262308; PIDN:AAB24637.1; PID:g262308
A;Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.
J. Biol. Chem. 264, 3822-3826, 1989
A;Title: Cleavage of type VII collagen by interstitial collagenase and A;Reference number: A30296; MUID:89139437; PMID:2537292
A;Accession: A30296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: I56328; MUID:93107742; PMID:1469284
A;Accession: I56328
                                                                                                                                                                                                                                                                                                                                                                                                                                           A/Cross-references: GB:L06862; NID:g388713; PIDN:AAA89196.1; PID:g3 R/Christiano, A.M.; Ryynaenen, M.; Uitto, J. Ryynaenen, M.; Uitto, J. Ryynaenen, M.; Uitto, J. Ryynaenen, M.; Uitto, J. Ryynaenen, R.;Christian, A.;S55, 1994
A/Title: Dominant dystrophic epidermolysis bullosa: identification A/Reference number: ASS255; MUID:94224777; PMID:8170945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hum. Mol. Genet. 2, 273-278, 1993
A;Title: The carboxyl-terminal half of type VII collagen, A;Reference number: I48103; MUID:93271985; PMID:8499916
A;Accession: I84686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 'A', 1240-1246, 'G', 1248-1250, 'XE', 1253-1255, 'Q', 1257, 'E'; 2032, 'C', 2034-2041; A; Note: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright, J. Invest. Dermatol. 99, 691-696, 1992
A;Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A;Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the (A;Reference number: S16316; MUID:91334380; PMID:1871109
A;Accession: S16316
                                                                                                                                                                                                                                                                                                                                                          A;Contents: annotation C;Comment: Prolines and lysines at the third ed and subsequently O-glycosylated.
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J. Biol. Chem. 269, 20256-20262, 1994
A;Tille: Cloning of human type VII collagen. Complete primary
A;Reference number: A54849; MUID:94327588; PMID:8051117
                                                                                                                                                                                                                                                                          A;Gene: GDB:COL7A1; EBR1; EBD1; EB
A;Cross-references: GDB:128750; OMIM:120120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: mRNA
A, Residues: 2395-2871, 'S', 2873-2944 <RE2>
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A;Experimental source: keratinocyte
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A; Residues: 815-892, 'E', 894-1439 < PAR>
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A;Residues: 'EFR',340-475,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,'C',
A;Cross-references: DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:BAA02853.1; PID:g453699
A;Experimental source: keratinocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Status: preliminary, translated from GB/EMBL/DDBJ
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(Cross-references: UNIPROT: Q02388; GB: L02870; NID: (Tanaka, T.) Takahashi, K.; Furukawa, F.; Imamura,
                                                                                                                                                                                                                                                                                                                              Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                       position
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Glanville, R.W.; Burgeson,
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                                                                             associated with hydroxylysine; !
                                                                                                                                                                                                                                                                                                                                                                                       tripeptide
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                            A;Molecule type: protein; mRNA
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F;954-1045/Domain: fibronectin type III repeat homology <PN9>
F;954-1045/Domain: fibronectin type III repeat homology <PN9>
F;1052-1219/Domain: von Willebrand factor type A repeat homology <VWA2>
F;1170-1172/Region: cell attachment (R-G-D) motif
F;1189-1253/Region: cill attachment (R-G-D) motif
F;1254-2783/Region: cell attachment (R-G-D) motif
F;2008-2010/Region: cell attachment (R-G-D) motif
F;2008-2010/Region: cell attachment (R-G-D) motif
F;253-255/Region: cell attachment (R-G-D) motif
F;253-255/Region: cell attachment (R-G-D) motif
F;253-255/Region: cell attachment (R-G-D) motif
F;253-255/Region: cell attachment (R-G-D) motif
F;253-255/Region: cell attachment (R-G-D) motif
F;253-255/Region: cell attachment (R-G-D) motif
F;253-255/Region: cell attachment (R-G-D) motif
F;253-255/Region: cell attachment (R-G-D) motif
F;253-255/Region: cell attachment (R-G-D) motif
F;267-294/Domain: carbohyd-terminal nonhelical #status predicted
F;237,786,1199/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
   DLV---DTAAQRLKGQGVKLFAVGIKNADPEELKRVASQPTSDFFFFVND-FSILRTLL
                                                                                                                                                GSGGDVIR-AIRELS--YKGGNTRTGAAILHVADHVFLPQLARPGVPKVCILITDGK-SQ 153
                                                                                                                                                                                                                         TEDREQIRQGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHE 112
                                                                                                                                                                                                                                                                                             DIVFLLDGSSSIGRSNFREVRSFLEGLVLPFSGAASAQGVRFATVQYSDDPRTEFGLDAL 97
                                                                                                                                                                                                                                                                                                                                                                     DLYFILDKSGSV-LHHWNEIYYFVEQLAHKF---ISPQ-LRMSFIVFSTRGTT---LMKL
                                                                        DIFFYSEREANRSRDIGAIVYCVGVKDFNETQLARIAD--SKDHVFPVNDGFQALQGII 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     von Willebrand
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            von Willebrand factor type A repeat homology fibronectin type III repeat homology <FN1> fibronectin type III repeat homology <FN2> fibronectin type III repeat homology <FN3> fibronectin type III repeat homology <FN3> fibronectin type III repeat homology <FN4> fibronectin type III repeat homology <FN5> fibronectin type III repeat homology <FN6>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bonds:
                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 102;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                              79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2944;
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208
                                                                                                                                                                                                                                                                                                                                                                             52
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A; Molecule type: mRNA
A;Residues: 467-546;550-595;752-764 <MOO>
A;Cross-references: GB:000185; GB:J00186
A;Note: the authors translated the codon TAC at 519 as Thr; tA;Mole; J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.E.
J. Biol. Chem. 259, 3407-3412, 1984
A;Title: Complete primary structure for the zymogen of human A;Reference number: A20751; MUID:84161997; PMID:6546754
A;Accession: A00934
                                                                                                                                                                                                                                                                         A;Reference number: A44622; MUID:83039428; PMID:6957884
A;Accession: A44622
                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P00751; EMBL:X72875; NID:g297568; PIDN: R;Woods, D.B.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982
A;Title: Isolation of cDNA clones for the human complement protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 19-Feb-1984 #Bequence revision 05-Aug-1994 #text change 09-Jul-2004
C;Accession: S34075; A44622; A09344; A19188; A19947; B19947; B25971; S14339;
R;Mejia, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G.
submitted to the EMBL Data Library, March 1993
A;Reference number: S34075
A;Accession: S34075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BBHU complement factor B precursor [validated] - human complement factor B precursor [validated] - human N;Alternate names: C3 convertase; C3 proactivator; glycine-rich N;Alternate value-romplement-pathway C3/C5 convertase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-764 < MEJ>
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                                                                   complement
                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:CAA51389.1;
olten, H.R.
                                                                                                                                                                 nucleic
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                                                                                                                                                                 acid translation
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A; Map posi
A; Introns:
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R;Niemann, M.A.; Bhown, A.S.; Miller, E.J.
Biochem. J. 274, 473-480, 1991
A;Title: The principal site of glycation of human complement Factor B.
A;Reference number: S14339; MUID:91174758; PMID:2006911
A;Accession: S14339
A;Molecule type: protein
A;Residues: 270-329 <NIE-
A;Note: binding site for carbohydrate to lysine under artificial conditions
R;Morley, B.J.; Campbell, R.D.
EMBO J. 3, 153-157, 1984
A;Title: Internal homologies of the Ba fragment from human complement components.
A,Cross-references: GDB:119726; OMIM:138470
A;Map position: 6p21.3-6p21.3
A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1;
                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:S67310; NID:g452937; PIDN:AAD13989.1; I R;Horiuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, Mol. Immunol. 30, 1587-1592, Particle: Human complement factor B: cDNA cloning, nucleotide: A;Reference number: I57824; MUID:94067177; PMID:8247029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 339-509 <CA1>
A;Cross-references: GB:J00126; NID:g187723; PIDN:AAA36226.1; PID:g553536
R;Wu, L.; McTley, B.J.; Campbell, R.D.
Cell 48, 331-342, 1987
A;Title: Cell-specific expression of the human complement protein factor
A;Reference number: A25971; MUID:87102880; PMID:3643061
                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-31, 'Q',
A; Cross-references: GI
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A;Residues: 16-225,'F',227-259 <MOR>
A;Residues: 16-225,'F',227-259 <MOR>
R;Schwaeble, W.; Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Busche Immunobiology 188, 221-232, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A44628; A; Accession: A44628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Amino acid sequence of the Bb fragment from complement factor B. Sequence A;Reference number: A19188; MUID:83204002; PMID:6342610
A;Contents: the final paper in a series documenting the sequence, glycosylation sit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-764 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-99 < WUL>
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A; Residues: 339-9
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A; Residues: 346-764 < CAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: nucleic acid translation differs from the sequence shown in A;Note: 736\text{-Ser} was also found
                                                                                               A;Gene: GDB:BF
                                                                                                                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                  Cross-references: GB:L15702; NID:g291921; PIDN:AAA16820.1; PID:g291922 Comment: 292-Cys has a free sulfhydryl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: GB:J00125
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                                                                                                                                                                                                               ,33-764 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUID:84158524; PMID:6323161
390/1; 424/1; 470/1;
502/3; 542/1;
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, S.; Volanakis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant zymogen
593/2; 619/1;
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   652/3;
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hypothetical protein C16E9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te C;Accession: T28797 R;Geisel, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;37-98/Domain: complement factor H repeat homology <FH1>
F;103-158/Domain: complement factor H repeat homology <FH2>
F;165-218/Domain: complement factor H repeat homology <FH3>
F;165-218/Domain: complement factor H repeat homology <FH3>
F;260-764/Product: C3/C5 convertase Bb fragment #status experimental <BBF>
F;268-458/Domain: von Willebrand factor type A repeat homology <VFA>
F;268-458/Domain: trypsin homology #status atypical <TRY>
F;482-752/Domain: trypsin homology #status atypical <TRY>
F;37-76,62-98,103-145,131-158,165-205,191-218,478-596,531-527,599-615,656-682,695-725/Diff;122,42,285,378/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;259-260/Cleavage site: Arg-Lys (complement factor D) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-567 <GEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid
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A; Note: gene is located in the major histocompatibility complex, class
C; Complex: complement factor B initially forms an inactive complex with
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                                                                                                                                                                                                                                                             A; Map position:
                                                                                                                                                                                                                                                                                        A; Gene: CESP:C16E9.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Function:
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                                                                                                             Matches
                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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   393
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Blakesley R.W., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT proc. Natl. Acad. Sci W S. accession of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the con
       Hillman R.T., Green R.E., Brenner S.E.;
"An unappreciated role for RNA surveillance.";
Genome Biol. 5:RESEARCHO08.1-RESEARCH008.16 (2004).
-!- FUNCTION: Cellular role is not yet known.
-!- SUBGUNIT: Binding does not occur in the presence of calcianthracis. Binding does not occur in the presence of calci-
-!- SUBCELULAR LOCATION: Type I membrane protein (Probable).
-!- ALTERNATIVE PRODUCTS:
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SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event-Alternative splicing, Named isoforms-4, Comment-Experimental confirmation may be la
                                                                                                                                                                                                                                                                                  IsoId=Q9H6X2-3;
                                                                                                                                                                                                                                                                                                                            IsoId=Q9H6X2-2; Sequence=VSP_000444,
                                                                                                                                                                                                                                                                                                                                                                                      codon
                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9H6X2-1;
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                                                                                                                                                                                                           SPECIFICITY:
                                                                                                                    =Q9H6X2-4; Sequence=VSP_000448, VSP_000449;
SPECIFICITY: Highly expressed in tumor endothelial of
in normal endothelial cells.
Binding to PA seems to be effected through the VWA
ITY: Belongs to the ATR family.
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Contains 1 VWFA domain.
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produced at very low levels due to a premature stop
e mRNA, leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sci. U.S.A. 100:5170-5174(2003).
                                                                                                                                                                                                                                                                               Sequence=VSP_000446,
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InterPro; IPR002035; VWF
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Pfam; PF05586; Anth C; 1.
Pfam; PF05586; Anth C; 1.
Pfam; PF00092; VWA; 1.
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; AK001463;
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                                                                                                                      EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFPVNDGFQALQGIIHSIL
                                                                                                                                                                   QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
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NEKPFSVEDTYLLCPAPILKEVGMKAALQV ->
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                                                                                                                                                                                                                                                              Score 899; DB 1
Pred. No. 1e-69;
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RA Okazaki Y., Furuno M., Kabukawa T., Adachi J., Bono H., Kondo S.,
RA Okazaki Y., Opato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Opato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Kawaji H., Kawasawa Y., Kodzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Kawasawa Y., Kodzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Kawasawa Y., Kodzierski R.M., King B.L.,
RA Kanaja A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Kanaja A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magjort D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Ponttus J.U., Qi D., Ramachandran S.,
RA Petrovsky N., Pillai R., Ponttus J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sample C.A., Setou M., Shimada K.,
RA Verardo R., Wanshawa Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vann Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Milming L.G., Wynshawa K., Arakawa T., Fikuda S.,
RA Milming L.G., Wankawa K., Arakawa T., Fikuda S.,
RA Milming L.G., Wankawa K., Sasaki K., Sasaki K., Sasaki K., Sasaki K., Sasaki K., Sasaki K., Sasaki K., Sasaki K., Sasaki K., Sasaki N., Sasaki N., Sasaki N., Sasaki N., Sasaki N., Sasaki N., Sasaki N., Sasaki N., Sasaki N., Sasaki N., Sasaki D., Shinagawa A.,
RA Nanishi A., Yanghino M., Waterston R., L
                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
-I- FUNCTION: Cellular role is not yet known.
-I- SUBUNIT: Binds to the protective antigen anthracis (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N.,
Kinzler K.W., St Croix B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Embryo
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Mus musculus (Mouse).
                                                                                                             or send
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                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the ATR family. SIMILARITY: Contains 1 VWFA domain.
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SIMILARITY: Bel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note No experimental confirmation DOMAIN: Binding to PA seems to be ef
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   AF378762;
AK013005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9CZ52-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9CZ52-2; Sequence=VSP_000450;
                                                                      is requires a license agreement (See http://www.isb-sib.lan email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxin receptor 1 precursor (Tumor endothelial marker
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BAB28591.1; ALT_INIT
                                       AAL11999.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: Type I membrane protein
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Gojobori T.,
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RESULT
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Best Local
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InterPro; IPRO0839; Ant C.
InterPro; IPRO082035; VWF A.
Pfam; PF05587; Anth Ig; I.
Pfam; PF05586; Anth C; 1.
Pfam; PF00092; VWA; I.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                                                                                         SEQUENCE FROM N.A. (ISOFORM 2).

MEDLINE=21539596; PubMed=11683410;

Bell S.E., Mavila A., Salazar R., Bayless K.J., K.

Maxwell S.A., Davis G.E.;

"Differential gene expression during capillary mo:
collagen matrices: regulated expression of genes:
membrane matrix assembly, cell cycle progression,
differentiation and G-procein signaling.";
J. Cell Sci. 114:2755-2773(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATR2 HUMAN STANDARD; PRT; 489 AA PS8335; Q86UI1; Q8NB13; Q96NC7; PSB-2003 (Rel. 41, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative SIGNAL
                     SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH ANTHRAX TO TISSUE=Placenta;
MEDLINE=22608610; PubMed=12700348; DOI=10.1073/pnas.0431098100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anthrax toxin receptor 2 precursor
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=ANTXR2; Synonyms=CMG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLYFILDKSGSVLHHWNEIYYFVEQLAHKFISPQLRMSFIVFSTRGTTLMKLTEDREQIR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EANRSRDLGAIVYCVGVKDFNETQLARIADSKDHVFFVNDGFQALQGIIHSIL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EANRSRDLGAIVYCVGVKDPNETQLARIADSKDHVFFVNDGFQALQGIIHSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGLEELQKVLPGGDTYMHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGLEELQKVLPGGDTYMHEGFERASEQIYYENRQGYRTASVIIALTDGELHEDLFFYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLYFILDKSGSVLHHWNEIYYFVEQLAHRFISPQLRMSFIVFSTRGTTLMKLTEDREQIR
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320
320
341
358
358
501
164
182
260
260
477
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    Rainey G.J.A., Bradley K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
                                                                   (ISOFORM 1), AND INTERACTION WITH ANTHRAX TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562
319
340
562
213
366
162
1182
260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 890; DB 1;
Pred. No. 6.3e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
GRCINPTRVENSQPAKYPLNNTYHPSSSPPAFIYTPPPPAP
HCPPPAPSAPTPPIPSPPSTLPPPPQAPPPNRAPPPSRPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPSV -> RFRGWRLTICLGSKHVHPGRHDKGPETPLLKQA
WMFSSFLERAFQ (in isoform 2).
/FTId=VSP_000450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; I
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FERASEQIYYENSQGYRTAS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asp/Glu-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6AC92049B4BB4F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                Bayless K.J., Kanagala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Capillary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor; Signal; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿
Young J.A.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (highly acidic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               morphogenesis
                                                                                                                                                                                                      morphogenesis
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                                                                                                                                                                                 involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIIALTDGELHEDLFFYSER
                                                                                                                                                               cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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A CHUITA Y., ADE K., KABILBATA N., KAIBURA N., SAIO N., TAILKAWA M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RI Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Nomila S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takamoto M., Kawakami B.,
RA Yumazaki M., Watanabe T., Sugiyama A., Takamoto M., Cawakami B.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwaza T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata R., Wakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Mateumura K., Nagase T., Namura N., Kikuchi H., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Wakagawa K.,
RA Nokumura K., Nagase T., Namura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
"Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wakamateu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E., Omura Y., Abe K., Kamihara K., Kaseuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishihashi T., Vamankir.
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Ota T., Suzuki Y., Nishikawa
                                                                                                                                                                                                    This SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human capillary receptor.";
                                                                                                                                                                 between
ween the Swiss-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is iffied and this statement is not removed. Usage by and folices requires a license agreement '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       following preference: calclum > manganese > magnesium > zinc.

Seems to bind to collagen type IV and laminin.

SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 2).

Secreted (isoform 3). Isoform 1 is expressed at the cell surface while isoform 2 is predominantly expressed at the cell surface.
                                                                                                                                                                                                                           Ilver, perturbed.

small intestine and spleen.

DOMAIN: Binding to PA seems to be effected through the VWA domain.

SIMILARITY: Belongs to the ATR family.

CTMTTARITY: Contains 1 VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              while isoform 2 is predominantly expressed reticulum and not at the plasma membrane. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Cellu
SUBUNIT: Binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Binds to the protective antigen (PA) of Bacillus anthracis in a divalent cation-dependent manner, with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                    Note=No experimental confirmation available; ISSUE SPECIFICITY: Expressed in colon, heart, ver, peripheral blood leukocytes, placenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note=No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P58335-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P58335-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P58335-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P58335-4; Sequence=VSP_008346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>4</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36:40-45(2004).
N: Cellular role is not yet known.
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.. Nishikawa T., Ots
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ental confirmation available;
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SEQUENCE FROM N.A.

STRAIN-C57BL/6; TISSUE-Bye;

MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler (
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.
                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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VARSPLIC
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                                                                                                     Mus musculus (Mouse)
                                                                                                                          Anthrax toxin
                                                                                                                                  25-OCT-2004 (TrEMBLrel. 25-OCT-2004 (TrEMBLrel.
                                                                                                                                                        Q6DFX2;
25-OCT-2004
                                                                                                                                                                            Q6DFX2
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PF00092; VWA; 1.
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                                                                                                                                                                                                                                                                                                                                                            Similarity
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489
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Rodentia;
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Last annotation update)
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Pred. No. 9.
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N-linked (GlcNAc. . .) (Potential)
Nishing (In isoform 2).
/FTId=VSP 008343.
TLDVSVSFNGGKSVISGSLIVTATECSNGIAAI
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/FTId=VSP_
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VSP 008345.
IEKELTA -> GRC
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Diatchenko L., Marusins K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bonsk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Matches 103
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InterPro; IPR008399; Ant C.
InterPro; IPR002035; VWF A.
Pfam; PP05587; Anth Ig; I.
Pfam; PP05586; Anth C; 1.
Pfam; PP00092; VWA; 1.
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Q8BVM2;
01-MAR-2003
                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933430J11 product:hypothetical Proline-rich region/von
Willebrand factor type A domain containing protein, full insert
                           SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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SEQUENCE
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Mammalia; Eutheria;
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GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                         Mus musculus
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      Hayashizaki Y.;
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TISSUE=Eye;
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59.5%;
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                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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1 J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE-Testis;

MEDLINE=20530913; PubMed=11076801; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

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Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

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Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.,

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                           EMBL; AK077206; BAC36683.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR008400; Anth Ig.
InterPro; IPR002035; VWF A.
Pfam; PF00587; Anth Ig; I.
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Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected
prepare full-length cDNA libraries for rapid discovery
Genome Res. 10:1617-1630(2000).
                                                                          Hypothetical protein SEQUENCE 641 AA;
                                                                                                                           PRINTS; PRO0453; VWFF
SMART; SM00327; VWA;
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STRAIN=C57BL/6J; TISSUE=Testis;
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the RIKEN Genome Exploration Research Group
TANALYSIS of the mouse transcriptome based o
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TISSUE=Testis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "High-efficiency full-length cDNA cloning.";
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420:563-573(2002).
                  Similarity
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                                                                                                                                             VWFADOMAIN
                                                                      70415 MW;
                  38.7%;
30;
                Score 348;
Pred. No. 9.
                                                                        199E300730BC85E3 CRC64;
 Mismatches
                                 DB 2;
                    8e-22;
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on functional annotation
                                 Length 641;
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"Cloning and characterization of integrin alpha subunits from solitary ascidian, Halocynthia roretzi.";

I Immunol. 166:1710-1715(2001).

C -!- SUBCELLULAR LOCATION: Type I membrane protein (By similaristic structure of the integrin alpha chain family. Belongs to the integrin alpha chain family. RMBL; AB048261; BAB21479.1; -.

R EMBL; AB048261; BAB21479.1; -.

R HSSP; P11215; 1BHQ.

R GO; GO:0005305; C:integral to membrane; IEA.

R GO; GO:0005305; C:integral to membrane; IEA.

R GO; GO:0005305; C:integral to membrane; IEA.

R GO; GO:0007229; P:protein binding; IEA.

R GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0007229; P:integrin-mediated
InterPro; IPR000413; Integrin_alpha.
InterPro; IPR002035; VWF_A.
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GO:0008305; C:integrin complex; IEA.
GO:0005515; F:protein binding; IEA.
GO:0007160; P:cell-matrix adhesion; IEA.
GO:00071299; P:integrin-mediated signaling pathway; IEA.
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  146 ARIA---DSKDHVFPVNDGFQALQGIIHSI 172
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SM00327; VWA; 1.
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                                                                                                                                             VGVVQYSHYVEGKSINKQKYITTEISIGEFKLLDNFENAVDRI----QLQGYTTYTGRALQ
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                                                                KVIRDFDDAYIGNKQVLLLLTDGQAKDNKLILP--NANRLRNKGIATFAVGVGEYDISEL
                                                                                                                                                                                                                              DVLFVLDGSGSVGKNFDKVKDWVKNIT-------AKLDIGKEIVR
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                        34; VWFA; 1.
Integrin; Signal; Transmembrane.
1 30 Potential.
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                                                                                                                                                                                                                                                                                                       Score 141; Ub 2,
Pred. No. 0.0023;
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                               -GDTYMHEGFERASEQIYYENRQGYRT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of rat alpha u, a "Submitted (AUG-1997) to the EMBL/GenBank/DDBu Garussell (AUG-1997) to the EMBL/GenBank/DDBu Garussell (AUG-1997) to the EMBL/GenBank/DDBu Garussell (AUG-1997) to the EMBL/GenBank/DDBu Garussell (AUG-1997) to the EMBL/GenBank/DDBu Garussell (AUG-1997) to the EMBL/GenBank/DDBu Garussell (AUG-1997) to the Submitter of ICAM3 and VCAM1. May play a role in the atherosclerotic process such as Clearing lipoproteins from plaques and in phagocytosis of blood-clearing lipoproteins from plaques and senescent erythrocytes horne pathogens, particulate matter, and senescent erythrocytes horne pathogens, particularity).
                                                           DOMAIN
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                                                                                                                                                                                                                                                  SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D associates with beta-2 (By similarity).
-:- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
-:- DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins with I-domains do not undergo protease cleavage.
-:- SIMILARITY: Belongs to the integrin alpha chain family.
-:- SIMILARITY: Contains 7 FG-GAP repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                       REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1185; INTEGRINA.
PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00191; Int_alpha; 5
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9QYE7;
Q5-JUL-2004 (Rel. 44, Created)
Q5-JUL-2004 (Rel. 44, Last sequence up
Q5-JUL-2004 (Rel. 44, Last annotation
                                                                                                                                                                                                                                                                                          Calcium;
                                                                                                                                                                                                                                                                                                              PROSITE; PS00242; INTEGRIN_ALPHA; PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00357; Integrin_alpha; 1.
Pfam; PF00092; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000413; Integr
InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley;
O'Brien M.M., VanderVi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01839; FG-GAP;
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                                                                                                                                                                                                                                                                 Signal;
                                                                                                                                                                                                                                                                                          Cell adhesion;
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                                                                                                                                                                                                                                                                   Transmembrane
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Rodentia;
                                                                                                                                Integrin_alpha.
                                                                                                                                                                                                                                                                                      Glycoprotein; Integrin; Magnesium;
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Potential.
Cytoplasmic (FG-GAP 1.
FG-GAP 2.
VWFA.
FG-GAP 3.
FG-GAP 4.
FG-GAP 5.
FG-GAP 5.
FG-GAP 7.
                                                                                                                                                                                                           Extracellular (Potential).
                                                                                                                                                                                                                                                    Potential.
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Q04588;
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                        InterPro;
Pfam; PFOC
Pfam; PFOC
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                                                 HSSP, P07996; ILSL.
HSSP, P07996; F:growth factor
GO; GO:0008083; F:growth factor
InterPro; IPR000762; PTN MK.
InterPro; IPR000884; TSPI.
InterPro; IPR002035; VWF_A.
                                                                                                                                                                       tenella microneme protein Mol. Biochem. Parasitol. 5 EMBL, M99058, AAA29076.1; PIR, A48569, A48569.
                                                                                                                                                                                                             MEDLINE=93149203; PubMed=8426611; DOI=10.1016/0166-6851(93)90255-V; Pasamontes L.E., Hug D., Huembelin M., Weber G.; Psequence of a major Elmeria maxima antigen homologous to the Elmer "Sequence of a major Elmeria maxima antigen homologous to the Elmer tenella microneme protein Etpl00."; Mol. Blochem. Parasitol. 57:171-174(1993).
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Major antige
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eimeria maxima.
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                      PF00090; TSP 1;
PF00092; VWA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen homologous
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      PR00453;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 26, Last annotation updat
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    VWFADOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence (emp100).
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MEDILINE=88257215; PubMed=2454931; DOI=10.1083/jcb.106.6.2153;

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homology to the alpha subunits of integrins.";
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01-OCT-1996 (Rel. 34, Last sequence up
25-OCT-2004 (Rel. 45, Last annotation
Integrin alpha-M precursor (Cell surfa
subunit) (CR-3 alpha chain) (CD11b) (I
(Neutrophil adherence receptor).
Name=ITGAM; Synonyms=CD11B, CR3A;
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SMART; SM00327; VWA; 1.
PROSITE; PS50092; TSP1; 5.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 724 AA; 75808 MW;
                                                                                                                                                MEDLINE=93123748; PubMed=8419480; Fleming J.C., Pahl H.L., Gonzalez D.A., Smith "Structural analysis of the CD11b gene and phy the alpha-integrin gene family demonstrate rem
                                                                                                     evolution.
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MEDLINE=89098893; PubMed=2563162;
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"Experimental support for a beta-propeller domain in integrin alpha-
subunite and a calcium binding site on its lower surface.";

Proc. Natl. Acad. Sci. U.S.A. 95:4870-4875 (1998).

-I- FUNCTION: Integrin alpha-M/beta-2 is implicated in various
adhesive interactions of monocytes, macrophages and granulocytes
as well as in mediating the uptake of complement-coated particles.

It is identical with CR-3, the toptake of complement of the third complement component. It probably recognizes the R-G-D
peptide in C3b. Integrin alpha-M/beta-2 is also a receptor for
fibrinogen, factor X and ICAM1. It recognizes Pl and P2 peptides
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MEDLINE=98362595; PubMed=9687375; DOI=10.1016/S0969-2126(98)00093-8; Baldwin E.T., Sarver R.W., Bryant G.L. Jr., Curry K.A., Fairbanks M.B., Finzel B.C., Garlick R.L., Heinrikson R.L., Horton N.C., Kelley L.L., Mildner A.M., Moon J.B., Mott J.E., Mutchler V.T., Tomich C.S., Watenpaugh K.D., Wiley V.H.; "Cation binding to the integrin CD11b I domain and activation model
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MEDLINE=95;71458; PubMed=7867070; DOI=10.1016/0092-8674(95)90517-0;
Lee J.O., Rieu P., Arnaout M.A., Liddington R.;
"Crystal structure of the A domain from the alpha subunit of integr
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MEDLINE=92144986; PubMed=1346576;
namerin A.G., Tenen D.G.;
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"The promoter of the CD11b gene directs myeloid-specific developmentally regulated expression.",
Proc. Natl. Acad. Sci. U.S.A. 88:10525-10529(1991).
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MEDLINE=96363671; PubMed=8747460; Discoll=10.1016/S0969-2126(01)00271-4;
Lee J.O., Bankston L.A., Arnaout M.A., Liddington R.C.;
"Two conformations of the integrin A-domain (I-domain): a pathway fo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92073318;
Shelley C.S., Arna
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Roth G.J.;
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"Experimental support fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3D-STRUCTURE MODELING OF 17-616.
MEDLINE=98226734; PubMed=9560195; DOI=10.1073/pnas.95.9.4870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activation?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 17-31. MEDLINE=87076671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "cDNA sequence for the alpha M subunit of the human neutrophil adherence receptor indicates homology to integrin alpha subunits.", Proc. Natl. Acad. Sci. U.S.A. 86:257-261(1989).
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                             granulocytes.
DOMAIN: The int
with I-domains
                                                                                                                       associates with beta-2.
SUBCELLULAR LOCATION: Type I membrane
TISSUE SPECIFICITY: Predominantly expi
                                                                                                                                                                                                                   of fibrinogen gamma chain.
SUBUNIT: Heterodimer of an alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80:631-638(1995).
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                             The integrin I-domain (insert)
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ressed in monocytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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SIMILARITY: Contains
DATABASE: NAME=PROW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                requires a license agreement (S
an email to license@isb-sib.ch).
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VWFA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
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Pfam; PF01839; FG-GAP; 3.
Pfam; PF00032; Integrin_alpha; 1
Pfam; PF00092; VWA; 1.
PRINTS; PR01185; INTEGRINA.
PRINTS; PR0453; VWPADOWAIN.
SMART; SM00191; Intealpha; 5.
SMART; SM00327; VWA; 1.
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Genew;
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GO:0007155;
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M18044;
J04145;
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LNA5; X-ray;
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PS00242;
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IPR002035; VWF_A.
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P:cell adhesion; TAS
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@=140-331.

@=143-334.

A=137-331.

A=144-337.

A=144-335.

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ITGAM.
INTEGRIN_ALPHA;
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Best Local Similarity
Matches 51; Conserv
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SIGNAL 1
CHAIN 17
                                                                                                                                                                                                                                                                                                                                                                                                       CAIC MOUSE STANDARD; PRT; 31
060847; P70322;
15-JUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence up
25-OCT-2004 (Rel. 45, Last annotation collagen alpha 1(XII) chain precursor.
                                                            Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R. Olsen B.R., Nishimura I.;
Olsen B.R., Nishimura I.;
"Structural variation of type XII collagen at its carboxyl-termin NC1 domain generated by tissue-specific alternative splicing.";
J. Biol. Chem. 274:22053-22059(1999).
-I- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrillar matrix (By similarity).
-I- SUBUNIT: Trimer of identical chains each containing 190 kDa contriple helical sequences (By similarity).
                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Skin fibroblast; MEDLINE=99348349; PubMed=10419532; DOI=1
                                                                                                                                                                                                                                                           Boehme K., Li Y., Oh P.S., Olsen B.R.; "Primary structure of the long and short splice variants of mouse collegen XII and their tissue-specific expression during embryoni
                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J, and Swiss Webster;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                      Name=Coll2al;
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50234; VWFA; 1.

3D-structure; Calcium; Cell adhesion; Direct protein sequencing; Glycoprotein; Integrin; Magnesium; Receptor; Repeat; Signal;
                                                                                                                                                                                                            AND XIIB-
                                                                                                                                                                                                                                                      development
                                                                                                                                                                                                                                                                                              MEDLINE=96170761;
                                                                                                                                                                                                                     PARTIAL SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090
                   ALTERNATIVE EXCUSED: Named 180forms=4; Event—Alternative splicing; Named 180forms=4; Comment—The final tissue form of collagen XII Comment—The final tissue form of the various
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IsoId=Q60847-1; Sequence=Displayed;
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1152
                                                                                                                                                                                                                                                                                               PubMed=8601036;
                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
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26.7%;
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                                                                                                                                                                                                                     AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 128.5; DB Pred. No. 0.024;
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                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                          DOI=10.1074/jbc.274.31.22053;
S.T., Karimbux N.Y., Taylor R
                                                                                                                                                                                                                                                                                                                               SPLICING (ISOFORMS
                                                                                                                                                                                                                                                                                                          TISSUE=Skin,
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                                                                                                                                                   carboxyl-terminal
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DR SWART; SM00060; FN3; 18.

DR SWART; SM00060; FN3; 18.

DR SWART; SM000210; TSPN; 1.

DR SWART; SM002210; TSPN; 18.

DR PROSITE; PSS0853; FN3; 18.

DR PROSITE; PSS0853; FN3; 18.

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INTERPRO; IPRO08160; Collagen.
InterPro; IPR008985; CONA like_lec_
InterPro; IPR003961; FN III.
INTERPRO; IPR008957; FN III-like.
INTERPRO; IPR003129; TSP N.
INTERPRO; IPR003129; WF_A.
INTERPRO; IPR003035; WMF_A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01391; Collagen; Pfam; PF00041; fn3; 18. Pfam; PF02210; TSP_N; 1. Pfam; PF00092; VWA; 4.
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EMBL; U57095; AAB07047.1; -.
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BKIN, CORNENTAL STAGE: The long NC3 XIIA isoforms are predominant at early stages (BD7 and 11); at later stages of development (ED15 and 17) the short NC3 XIIB forms become the major forms. As the short NC3 forms become the major product, the long splice variant continues to be expressed in several tissues, even after birth. The long NC1 isoforms, XIIA-1 and XIIB-1, peak in 15-day old embryos and decrease in 17-day old ones. The expression of the short NC1 form XIIB-2 remains constant throughout late stages of embryonic development (ED15 and ED17).

PTM: The triple-helical tail is stabilized by disulfide bonds at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains (By)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: O-glycosylation of isoform
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Y: Highest expression in tendons,
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Cell attachment site (Potential).
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N-linked (GlcNa)
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Pred. No. 0.076;
4; Mismatches
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Missing (In isoform XIIB-2).
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EPY -> GSG (in is
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Triple-helical region (COL1)
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Triple-helical region (COL2)
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W; 9B1F999C86AB3251
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Proximal thread matrix protein 1 variant a.
Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloidea; Mytildae; Mytilus.
NCBI_TaxID=6550:
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Proximal thread matrix protein 1b.
Mytilus edulis (Blue mussel).
Eukaryota, Metazoa, Mollusca; Bivalvia; Pteriomorph
Mytiloidea; Mytilidae; Mytilus.
MCBI_TaxID=6550;
                                          MEDLINE-22313036; PubMed-12425661; DOI=10.1021/bm0255903; Sun C., Lucas J.M., Waite J.H.; "Collagen-binding matrix proteins from elastomeric extraobyssal fibers.";
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SMART; SM00327; VWA; 2.
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MBL; AY053390; AAL17973.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
Weognathae; Galliformes; Phasianidae; Phasianinae;
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             AND ALTERNATIVE
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EMBL; D00824; BAA00701.1; EMBL; K61024; CAA43358.1; EMBL; M17375; AAA48718.1; EMBL; J05137; AAA487635.1; EMBL; X67327; CAA47744.1; PIR; A40020; A40020. HSSP; P56199; 1QC5.
InterPro; IPRO08160; C
InterPro; IPRO08985; C
InterPro; IPRO03961; F
InterPro; IPRO03129; T
InterPro; IPRO03129; T
InterPro; IPRO02035; V
Pfam; PP001391; Collage
Pfam; PP001391; Collage
Pfam; PP00210; TSP_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is proud between the Swiss Institute of Bioinformatics between the Swiss Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Large and small splice variants of collagen XII: differential expression and ligand binding.";
J. Cell Biol. 130:1005-1014(1995).
-!- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrillar matrix.
-!- SUBUNIT: Trimer of identical chains each containing 190 kDa contribute PRODUCTS:
-- FUNCTIONATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement entities requires a license
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93042014; PubMed=1420368; DOI=10.1016/0167-4781(92)90145-P; Trueb J., Trueb B.; "The two splice variants of collagen XII share a common 5' end."; Blochim. Blophys. Acta 1171:97-98(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId-Pl3944-2; Sequence=VSP 001148; TISSUE SPECIFICITY: Type XII collagen is present in t ligaments, perichondrium, and periosteum, all dense c tissues containing type I collagen. DOMAIN: This sequence defines five distinct domains, DOMAIN: This sequence domaines and three nontriple-helical domains (COL1 and COL2) and three nontriple-homains (NC1, NC2, and NC3).

PTM: The triple-helical tail is stabilized by disulfi
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buropean Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
ified and this statement is not removed. Usage by an
ities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 18 fibronectin type III SIMILARITY: Contains 1 TSP N-terminal (TSPN) SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interrupted helices (FACIT) family.
SIMILARITY: Contains 18 fibronectin
SIMILARITY: Contains 1 TSP N-termin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similar: SIMILARITY:
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Comment=The final tissue form of collagen XII may contain
homotrimers of either isoform Long or isoform Short or any
combination of isoform Long and isoform Short. Only isoform Long
is a proteoglycan. Isoform Long has more restricted expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unit (G-X-Y) are hydronylated;
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FN_III-like.
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fn3; 1: TSP_N; VWA; 4 Collagen;

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SMART; SM00060; FN3; 18.
SMART; SM00210; TSPN; 1.
SMART; SM00321; VWA; 4.
SMART; SM00327; VWA; 4.
PROSITE; PS50853; FN3; 18.
PROSITE; PS50854; VWFA; 4.
Alternative splicing; Cell adhesion; Collagen;
Alternative splicing; Extracellular matrix; Glycoprotein;
Hydroxylation; Repeat; Signal; Structural protein.
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Pred. No. 0.19
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Fibronectin
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Fibronectin
Fibronectin
                                Score 125;
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Potential.
Collagen alpha 1(XII) chain.
Fibronectin type-III 1.
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O-linked (X
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Cell attachment site (Potential).
N-linked (GlNAc. .) (Potential).
O-linked (Xyl. .) (chondroitin su
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Triple-helical region (
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Triple-helical region (COL2)
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     74;

    .) (chondroitin sulfate)

    chondroitin

                                  Length 3124;
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Short).
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ID ITAD HUMAN STANDARD;
AC Q13349; Q15575; Q15576;
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Best Local S
Matches 41
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Mol. Biochem Parasitol. 107:3
EMBL; AF061273; AAF01565.1; -.
HSSP; P07996; 1LSL.
GO; GO:0008083; F:growth facto
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SEQUENCE FROM N.A.

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MEDLINE=20183852; PubMed=10717300; DOI=10.1010...

Lovett J.L., Howe D.K., Sibley L.D.;

Lovett J.L., Howe D.K., Sibley L.D.;

"Molecular characterization of a thrombospondin-related anonymous protein homologue in Neospora caninum.";

Parasitol. 107:33-43(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00209; TSP1; 6.
SMART; SM00327; VWA; 1.
PROSITE; PS00141; ASP PROTEASE; UNKNOWN_1.
PROSITE; PS50092; TSP1; 2.
PROSITE; PS50234; VWFA; 1.
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Q9UBJ9; O1-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Thrombospondin-related adhesive protein homolog.
Name=MIC2;
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                                                                                                                                                                                                                                                                                                                                                                                                            h 13.8%; So
Similarity 27.5%; Po
41; Conservative 27;
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                                                                                                                                                                 ELHEDLFFYSERBANRSRDLGAIVYCVGV
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                                                                                                                         BSDSD--FHTVNEAKVIRERGGIITVLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08083; Figrowth factor activity; IEA.
IPR001969; Pept Asp AS.
IPR000762; PTN MK.
IPR000884; TSPI.
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 124; DB
Pred. No. 0.03
27; Mismatches
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1162
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16-OCT-2001
05-JUL-2004
Integrin alpi
                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWAL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                         ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- FUNCTION: Integrin alpha-D/beta-2 is a receptor for ICAM3 and VCAM1. May play a role in the atherosclerotic process such as clearing lipoproteins from plaques and in phagocytosis of bloodborne pathogens, particulate matter, and senescent erythrocytes from the blood.

-I- SUBUNIT: Heterodimer of an alpha and a beta subunit. Alpha-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Van der Vieren M., Crowe D.T., Hoekstra D., Vazeux R. Grayson M.H., Bochner B.S., Gallatin W.M., Staunton I. "The leukcyte integrin alpha D beta 2 binds VCAM-1: binding interface between I domain and VCAM-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99059842; PubMed=9841932;
Grayson M.H., Van der Vieren M., Sterbinsky S.A., Michae
Hoffman P.A., Staunton D.E., Bochner B.S.;
"alphadbeta2 integrin is expressed on human eosinophils
an alternative ligand for vascular cell adhesion mole
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"Cloning and chromosomal localization
beta 2-integrin alpha subunit.";
Gene 171:291-294(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WEDLINE=96111956; PubMed=8777714; DOI=10.1016/1074-7613(95)90058-6; Wan der Vieren M., Le Trong H., Wood C.L., Moore P.F., St John T., Staunton D.E., Gallatin W.M., Staunton D.E., Gallatin W.M., Panovel leukointegrin, alpha d beta 2, binds preferentially to ICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99370002; PubMed=10438935;
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MEDLINE=20187620; PubMed=10722744; DOI=10.1074/jbc.275.12.8959;
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                                                                                                                                                                                ASSOCIATES WITH Deta-2.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Expressed moderately on myelomonocytic cell

lines and subsets of peripheral blood leukocytes and strongly on

tissue-specialized cells, including macrophages foam cells within

atherosclerotic plaques, and on splenic red pulp macrophages.

DOMAIN: The integrin I-domain (insert) is a VWFA domain. Integrins

with I-domains do not undergo protease cleavage.

SIMILARITY: Belongs to the integrin alpha chain family.

SIMILARITY: Contains 1 VWFA domain.
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Catarrhini; Hominidae;
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  (See http://www.isb-sib.ch/announce,
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GO; GO:0007160; P:cell-matrix adhesion; NAS.
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